GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

- protein search, using sw model OM protein February 23, 2006, 07:43:54 ; Search time 38 Seconds
(without alignments)
238.010 Million cell updates/sec Run on:

US-09-688-566-81 Perfect acore: Title:

494 1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKYDDPISINYRT Sequence:

94

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	님	fibronectin precur	fibronectin - bovi	fibronectin precur	fibronectin - chic	fibronectin - chic	fibronectin - Afri	probable tenascin	tenascin-X - bovin	restrictin precurs	tenascin precursor	janusin precursor,	tenascin-X precurs	leukocyte antigen-	tenascin precursor	cytotactin - chick	tenascin precursor	$\overline{}$	tenascin-C - human	tenascin-X - pig (5	tenascin - eastern		collagen alpha 1(X	undulin 1 - human	protein-tyrosine-p	protein-tyrosine-p	fibronectin, trans	protein-tyrosine-p	fibronectin - chic
SUMMARIES	ΩI	FINHU	FNBO	S14428	A28512	A29355	A43908	T09070	T42629	JH0675	S19694	A45445	A40701	S46216	JQ1322	A31930	A32230	A54849	A32160	S65944	A56178	A43902	A56493	A40020	A40970	D54689	C54689	S00848	I50213	S71465
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de	Query Match	73.1	71.7	67.4	63.0	63.0	53.0	25.3	25.1	24.5	24.5	23.5	22.5	22.4	22.3	21.9	21.9	21.6	21.3	20.6	20.2	19.9	19.4		19.0		18.6			17.9
	Score	361	354	333	311	311	262	125	124	121	121	116	111	110.5	110	108	108	106.5	105	102	100	98.5	96	96	94	92	92		90.5	88.5
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tenascin - rat (fr fibronectin ED-B - leukocyte antigen-	protein-tyrosine-p tenascin-X - mouse fibronectin BD-A - neohrin - human	type XII collagen collagen alpha 1(X collagen alpha 1(X	collagen alpha 1(X tenascin Y precurs protein-tyrosine-p	protein-tyrogine-p undulin 2 - human hypothetical prote
A54861 I46162 TDHULK	A55148 148839 146161 T37190	151027 A45974 S31212	S78476 T42635 TDFFLK	138670 B40970 A90255
994	4000	000	777	777
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321	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	3 3 3 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 2 1 2 2	4 4 4 6 4 6

ALIGNMENTS

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SULT	į

fibronectin precursor [validated] - human
N.Alternate names: fibronectin splice form ED-A
C;Species: Homo Sapiens (man)
C;Species: Homo Sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2004
C;Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22
R;Dean, D.C.; Bowlus, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A;Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A;Reference number: A26460; MUID:87175578; PMID:3031656

A,Molecule type: DNA
A,Residues: 1-49 <DEA>
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A,Cross-references: UNIPROT:P02751; UNIPROT:Q14327; UNIPARC:UPI000016A926; GB:M15801; NI
R;Oldbers: R. Rucelahti, B.
J. Biol. Chem. 261, 2113-2116, 1986
A;Title: Evolution of the fibronectin gene.
A,Reference number: A26284; MUID:86111901; PMID:3003095

A;Accession: A26284

A; Molecule type: DNA A; Residues: 1447-1540 <old>
A; Residues: 1447-1540 <old>
A; Cross-references: UNIPARC: UP10000112E37; GB:M12549; NID:g182688
A; Note: the authors translated the codon TTC for residue 1494 as Glu
R; Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
R; Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
A; Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B
A; Reference number: S00848; MUID:88233940; PMID:3375063

A; Accession: S03917

A; Molecule type: DNA A; Residues: 1554-1767, 'V',1769-1783 < PAO> A; Residues: 1554-1767, 'V', 1769-1783 < PAO> A; Cross-references: UNIPARC:UP1000017432B; EMBL:X07718; NID:g31402 A; Note: the authors translated the codon AAC for residue 1631 as Asp R; Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E. R; Vibe-Pedersen, R.; Magnusson, S.; Baralle, F.E. A; Title: Donor and acceptor splice signals within an exon of the human fibronectin gene: A; Reference number: A24854; MUID:87030929; PMID:3770201

A; Accession: A24854

A; Residues: 1992-2147 <VIB>
A; Residues: 1992-2147 <VIB>
A; Residues: 1992-2147 <VIB>
R; Cross-references: UNIPARC: UPI000017432C; GB: X04530; NID: 931436
R; Gutman, A.; Yamada, K.M.; Kornblihtt, A.
FBBS Lett. 207, 145-148-1986
A; Title: Human fibronectin is synthesized as a pre-propolypeptide.
A; Reference number: A24476; MUID: 87030890; PMID: 3770189

A;Accession: A24476 A;Status: not compared with conceptual translation

A;Molecule type: mRNA
A;Residues: 1-14,'Q',16-38 <GUT>
A;Residues: 1-14,'Q',16-38 <GUT>
A;Crose-references: UNIPARC:UPI000017432D
R;Kornblihtt, A.R.: Unezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985

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A; Cross-references: GDB:119135; OMIM:135600
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,Residues: 616-677,'Q',679-703,'PT' <CAL>
,Cross-references: UNIPARC:UPI0000174339
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A; Residues: 2071-2080;2112-2356 <GAR4>
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A, Cross-reference: UNIPARC:UPI000017432F; UNIPARC:UPI0000174330; GB:X00739
B, Accession: A2101
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A; Residues: 1978-1990, 2016-2018, NV, 2020-2081, 2113-2127 <SEK>
A; Residues: 1978-1990, 2016-2018, NV, 2020-2081, 2113-2127 <SEK>
A; Cross-references: UNIPARC:UP100000664C; GB: M44060; NID: GB182701; PIDN:AAA52464.1; PID: R; Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.

Proc. Natl. Acad. Sci. U.S.A. 80, 3218-322, 1983
A; Title: Isolation and characterization of cDNA clones for human and bovine fibronectine A; Reference number: A21165; MUD: 83221567; PMID: 6304699
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 2291-2386 <KO3>
A; Residues: 2291-2386 <KO3>
A; Residues: 2291-2386 <KO3
A; Paralite: Paralo; N. Pearlstein, B.; Prangione, B.
A; Title: Primary structure of human plasma fibronectin.
A; Reference number: A92398; MUD: 84032463; PMID: 6630202
                                                                                                                                                                                                                                                                        A;Residues: 32-1344,1346-2080;2112-2386 <KOR>
A;Cross-references: UNIPARC:UP1000017432F; UNIPARC:UP1000017432F; GB:X02761
A;Cross-references: UNIPARC:UP1000017432F; UNIPARC:UP1000017432F; GB:X02761
A;Roznblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A;Reference number: A93529; MUID:84272258; PMID:6462919
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A,Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GAR1>
A;Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GAR1>
A;Cross-references: UNIPARC:UPI0000174335
R;Garcia-Pardo, A.; Gold, L.I.
Arch. Blochem. Blophys. 304, 181-188, 1993
A;Title: Further characterization of the binding of fibronectin to gelatin reveals the A;Reference number: 834791; MUID:93312001; PMID:8323285
                            at
A;Title: Primary structure of human fibronectin: differential splicing may generate A;Reference number: A91008; MUID:85284965; PMID:2992939
A;Accession: A91008
A;Status: nucleic acid sequence not shown
A;Wolecule type: mRNA
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Ajaccession: A60904
Ajmolecule type: protein
Ajresius: 293-301 cGRI>
Ajritle: Primary structure of a DNA- and heparin-binding domain (domain III) in human ple Ajreference number: A23901; MUD:86008277; PMID:3900070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UP10000174339

Piblarschbacher, M.D.; Ruoslahti, B.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982

A;Title: The cell attachment domain of fibronectin. Determination of the primary structum A;Reference number: A92386; MUID:82265604; PMID:7050098
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1, Rosidues 1589-17.1722-2058 «GAR3»

1, Rosidues 1589-17.1722-2058 «GAR3»

1, Tressel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pandel

1, Tressel, T.; McCarthy, J. 1991

1, Title: Human plasma fibronectin. Demonstration of structural differences between the A-

1, Reference number: S14357; MUID:91190085; PMID:2012601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
. Biol. Chem. 260, 10320-10325, 1985
.Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dalti
.Reference number: A23891; MUID:85261459; PMID:4019516
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A.Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
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F;1-26/Domain: signal sequence #status predicted <8RO>
F;2-31/Domain: signal sequence #status predicted <RRO>
F;2-236/Pomain: fibronectin #status experimental <MAT>
F;52-272/Domain: fibronectin type I repeat homology <1F2>
F;97-135/Domain: fibronectin type I repeat homology <1F3>
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F;186-225/Domain: fibronectin type I repeat homology <1F5>
F;30-608/Domain: collagen binding <CBR>
F;30-608/Domain: fibronectin type I repeat homology <1F6>
F;30-608/Domain: fibronectin type I repeat h
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C;Comment: The extra domain and connecting strand 3 are subject to developmental and tis
C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins, attion, and transformation.
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A,Molecule type: protein
A,Residues: 1441-1548 <PIE>
A,Cross-references: UNIPARC:UPI0000141CD5
A,Cross-references: UNIPARC:UPI0000141CD5
A,Note: residues: 1524-1527 are responsible for the cell-binding activity
B,Garcia-Pardo, A, Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A,Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa A,Reference number: A32517; MUID:87241275; PMID:3593230
A,Accession: A32517
A;Residues: 291-300;551-560 <GAR2>
A;Cross-references: UNIPARC:UPI0000174336; UNIPARC:UPI0000174337
B;GTiffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
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GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT
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A; Readdues: 1-16, 'C', 18-20, 'S', 22-412;447-463;1367-1517;1567-1673;2062-2176, 'N', 2178-226
A; Cross-references: UNIPARC: UPI000017433E; UNIPARC: UPI000017439C;
C; Comment: The plasma fibronectin molecule consists of two chains, which are connected by C; Comment: The plasma fibronectin molecule consists of two chains, which are connected by C; Comment: Plasma fibronectin spand synthesized by hepatocytes.
C; Comment: Plasma fibronectin is synthesized by hepatocytes.
C; Comment: Plasma fibronectin from type I repeat homology; fibronectin type I repeat homology is collagen binding; duplication; extracellu F; 21-241/Domain: fibronectin type I repeat homology <1F2>
F; 21-56, Domain: fibronectin type I repeat homology <1F2>
F; 21-54, Domain: fibronectin type I repeat homology <1F2>
F; 21-244/Domain: fibronectin type I repeat homology <1F2>
F; 21-244/Domain: fibronectin type I repeat homology <1F2>
F; 21-241/Domain: fibronectin type I repeat homology <1F3>
F; 21-241/Domain: fibronectin type II repeat homology <1F3>
F; 21-241/Domain: fibronectin type III repeat homology <1F3>
F; 21-241/Domain: fib
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A;Mesidues: 1-2265 csRO.
A;Residues: 1-2265 csRO.
A;Cross-references: UNIPROT:P07589; UNIPARC:UP1000012A7BB
R;Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc., Natl. Acad. Sci. U.S.A. 86, 23124-3322, 1988
A;Title: Isolation and characterization of CDNA clones for human and bovine fibronectins
A;Reference number: A21165; MUID:83221567; PMID:6304699
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A; Residues: 2170-2265 KOR>
A; Residues: 2170-2265 KOR>
A; Cross-rences: UNIPARC: UPI000016C30C; GB: K00800; NID: g163055; PIDN: AAA30521.2; PID: A; Petersnei, T.B.; Thogersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983
A; Title: Partial primary structure of bovine plasma fibronectin: three types of internal A; Reference number: A23292; MUID:83117805; PMID:6218503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26452; B21165; Ā23292
C;Accession: A26452; B21165; Ā23292
Bur. J. Biochem. 161, 441-453, 1986
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                                                                                                                                                                                                                                                                 Score 361; DB 1; Length 23
Pred. No. 1.8e-28;
4; Mismatches 17; Indels
F;360-401/Domain: fibronectin type II repeat homology <2F1:
F;420-461/Domain: fibronectin type II repeat homology <2F2:
F;470-508/Domain: fibronectin type I repeat homology <1F7:
F;518-555/Domain: fibronectin type I repeat homology <1F9:
F;561-599/Domain: fibronectin type I repeat homology <1F9:
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                                                                                                                                                                                                                                                                 73.18;
77.78;
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Best Local Similarity 77.7
Matches 73; Conservative
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Fig. Cross-link: isopeptide (Gln) (interchain to Lys Mc amino experime experime F;3/Cross-link: isopeptide (Gln) (interchain to Lys Mc amino experime F;21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-3 7,2155-2167,2174-2200,2198-2209,Disulfide bonds: #status predicted F;399,497,511,846,976,1213,1987/Binding site: carbohydrate (Asn) (covalent) #status absent F;1494,1944/Binding site: carbohydrate (Thr) (covalent) #status absent F;244/Binding site: carbohydrate (Thr) (covalent) #status experimental F;2246/Disulfide bonds: interchain (to 2250) #status predicted F;2250/Disulfide bonds: interchain (to 2266) #status predicted
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A;Residues: 1-2477 (HTN>
A;Cross-references: UNIPROT:P04937; UNIPPAC:UPI000012A7C6; EMBL:X15906; NID:g56163; PIDN
R;Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A;Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A;Reference number: S12455; MUID:88054951; PMID:2445560
A;Status: nucleic acid sequence not shown
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A;Cross-references: UNIPARC:UP10000177ARA; EMBL:X15906
A;Cross-references: UNIPARC:UP10000177ARA; EMBL:X15906
B;Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A;Title: A single rat fibronectin gene generates three different mRNAs by alternative sp A;Reference number: A22319; MUID:84298097; PMID:6089177
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C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
R;Hynes, R.O.
B;Hynes, R.O.
A;Reference number: S14428
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F;1055-1134/Domain: fibronectin type III repeat homology <FN35-
F;1142-1227/Domain: fibronectin type III repeat homology <FN36-
F;1326-1404/Domain: fibronectin type III repeat homology <FN36-
F;1326-1404/Domain: fibronectin type III repeat homology <FN31-
F;1410-1517/Domain: cell attachment <CAD>
F;1493-1495/Region: cell attachment (R-G-D) motif
F;1491-1592/Domain: fibronectin type III repeat homology <FN31-
F;160-1807/Oomain: hoparin binding <fN32-
F;160-1687/Domain: fibronectin type III repeat homology <FN31-
F;160-1687/Domain: fibronectin type III repeat homology <FN31-
F;1670-1977/Region: cell attachment (R-G-D) motif
F;1982-2062/Domain: fibronectin type III repeat homology <FN3N-
F;1988-2216/Domain: fibronectin type III repeat homology <FN3N-
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2130-2167/Domain: fibronectin type I repeat homology <1F11>
2174-2209/Domain: fibronectin type I repeat homology <1F12>
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A; Accession: A29355
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Rifalkenberg, C.; Enghild, J.J.; Thogersen, I.B.; Salvesen, G.; Akerstroem, B. Blochem. J. 301, 745-751, 1994

A/Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in A, Reference number: S46203

A/Accession: S56203

A/Accession: S56203

A/Accession: S56203

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R;Odermatt, E.; Tamkun, J.W.; Hynes, R.O.
R;Odermatt, E.; Tamkun, J.W.; Hynes, R.O.
A;Odermatt, Acad. Sci. U.S.A. 82, 6571-6575, 1985
A;Title: Repeating modular structure of the fibronectin gene: Relationship to protein A;Reference number: 159049; MUID:86016741; PMID:3863113
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fibronectin type I repeat homology <1F10>
fibronectin type I repeat homology <1F11>
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A;Molecule type: mRNA
A;Residues: 1586-1720,'T',1722,1813-2477 <SC2>
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A,Status: translated from GB/EMBL/DDBJ
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Cyaccession: A28512
Rykubomura, S.; Obara, M.; Karasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, K Bicchim. Biophys. Acta 910, 171-181, 1987.

Rykubomura, S.; Obara, M.; Karasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, K A; Title: Genetic analysis of the cell binding domain region of the chicken fibronectin gel A; Reference number: A28512; MUID:88050950; PMID:2823899

A; Residues: 1-273 «KUB»

A; Residues: 1-274 «KUB»
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R;Norton, P.A.; Hynes, R.O.
Mol. Cell. Biol. 7, 4297-4307, 1987
A;Title: Alternative splicing of chicken fibronectin in embryos and in normal and transfic A;Reference number: A29355; MUID:88142820; PMID:2830487
                                          F;53-79,77-88,98-126,124-136,142-170,168-180,187-216,214-226,232-261,259-271,308-335,333

88,2366-2378,2385-2411,2409-2420/Disulfide bonds: #status predicted

F;2458/Disulfide bonds: interchain (to 2462) #status predicted

F;2462/Disulfide bonds: interchain (to 2458) #status predicted
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A28512
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C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRITYGETGGNSPVQEF1
                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1020 <NOR>
A; Cross-treferences: UNIPROT:P11722; UNIPARC:UP10000177AES
C; Genetics:
F;2385-2420/Domain: fibronectin type I repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||| |||||:|||| : |:
1597 NIKPGADYTITLYAVTGRGDSPASSKPVSINYQT 1630
                                                                                                                                                                                                                                                                                                            Score 333; DB 2;
Pred. No. 1.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
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                                                                                                                                                                                                                                                                                                                 67.4%;
68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eibronectin - chicken (fragment)
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.13
Matches 64; Conservative
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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A;Accession: A53908
A;Accession: A53908
A;Accession: A543908
A;Accession: A54308
A;Accession: 
                duplication; extracellular matrix; glycoprotein; heter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribesimone, D.W.; Norton, P.A.; Hynes, R.O.
Dev. Biol. 149, 357-369, 1992
A;Title: identification and characterization of alternatively spliced fibronectin mRNAs
A;Reference number: A43908; WUID:92111942; PMID:1730390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 VSDVPRDLEVNPTSPTSLEISWDAPAVTVRYYRIITYGETGGSSPVQEFTVPGTMSRATIT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRIIYGEIGGNSPVQEFTVPPWASIATIS 60
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
C;Accession: A43908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
C; Keywords: alternative splicing; duplication; extracellular matr: F; 1-86/Domain: fibronectin type III repeat homology <FW3H> F; 92-177/Domain: fibronectin type III repeat homology <FW3I> F; 180-262/Domain: fibronectin type III repeat homology <FW3I> F; 257-259/Region: cell attachment (R-G-D) motif F; 274-356/Domain: fibronectin type III repeat homology <FW3K> F; 364-446/Domain: fibronectin type III repeat homology <FW3K> F; 364-36/Domain: fibronectin type III repeat homology <FW3I> F; 456-628/Domain: fibronectin type III repeat homology <FW3I> F; 566-628/Domain: fibronectin type III repeat homology <FW3I> F; 837-917/Domain: fibronectin type III repeat homology <FW3I> F; 840-979/Domain: fibronectin type III repeat homology <FW3I> F; 940-979/Domain: fibronectin type III repeat homology <FW3IPO F; 940-979/Domain: fibronec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.0%; Score 311; DB 2; Length 1020; 64.9%; Pred. No. 9e-24; ive 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLKPGVDYTITVYAVTGRGDSPASSKPVTVTYKT 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 64.9%;
61; Conservative 1
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Matches 61; Conserv
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F;2197-2277/Domain: fibronectin type III repeat homology <FN3Q>
F;2197-2240/Domain: fibronectin type I repeat homology <FR10>
F;2246-2283/Domain: fibronectin type I repeat homology <1F10>
F;2246-2283/Domain: fibronectin type I repeat homology <1F12>
F;2360-2425/Domain: fibronectin type I repeat homology <1F12>
F;55-81,79-90,100-128,126-138,144-172,170-182,189-218,216-228,234-263,261-273,309-336,33
Z33,2371-2383,2390-2416,2414-2455/Disulfide bonds: #status predicted
F;2459/Disulfide bonds: interchain (to 2463) #status predicted
F;2463/Disulfide bonds: interchain (to 2459) #status predicted
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A; Map position: 17
A; Introns: 124(1; 713/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15
019/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3
C; Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type C; Keywords: extracellular matrix
C; Keywords: extracellular matrix
F; 826-906/Domain: EGF homology * EGF>
F; 826-906/Domain: fibronectin type III repeat homology < 3FR>
F; 3789-3997/Domain: fibrinogen beta/gamma homology < FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-4006 <ROW>
A;Cross-references: UNIPROT:035452; UNIPARC:UPI000002A159; EMBL:AF030001; NID:92564945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: T09070
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: 216543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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N;Alternate names: flexilin
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ČiSpecies: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             828 DGPQDLRVVAVTPTTLDLSWLRPQAEVDRFVVSY-VSAGNQRVR-LEVPPEADRTQLTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VSDVPRDLEVVAATPTSRLISMNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
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                                                                                                                                                                                                                                                                                                                                                                  53.0%; Score 262; DB 2; Length 2481;
llarity 53.2%; Pred. No. 2.6e-18;
Conservative 16; Mismatches 28; Indels (
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R;Elefteriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, J. Biol. Chem. 272, 22866-22874, 1997
A;Title: Characterization of the bovine tenascin-X.
A;Reference number: Z22180; MUID:97426436; PMID:9278449
A;Accession: T42629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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SC

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C;Accession: S19694
R;Nishi, T.; Weinstein, J.; Gillespie, W.W.; Paulson, J.C.
R;Nishi, T.; Weinstein, J.; Gillespie, W.M.; Paulson, J.C.
A;Title: Complete primary structure of porcine tenascin. Detection of tenascin transcrip A;Reference number: S19694; WUID:92104189; PMID:1722152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1746 <NIS.
A; Residues: 1-1746 <NIS.
C; A; Cross-references: UNIPROT: Q29116; UNIPARC: UPI0000136BBB; EMBL: X61599; NID: 92124; PIDN: C; Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type I C; Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type I C; Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracelly F; 1-22/Domain: signal sequence #status predicted <SIG> F; 23-1746/Product: tenascin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydrate (Asn) (covalent) #sta
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Nichtenate names: neural recognition glycoprotein J1-160/180, short form
Nichtenate names: neural recognition glycoprotein J1-160/180, short form
Nichtenate: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A45445; B45445; B32023
R;Puss, B; Wintergerst, Es; Bartsch, U; Schachner, M.
Cell Biol. 120, 1237-1249, 1993
A;Title: Molecular characterization and in situ mRNA localization of the neural recognit.
A;Reference number: A45445
A;Reference number: A45445
A;Status: preliminary
A;Rocession: A45445
A;Status: preliminary
A;Rocession: L1356 *FUS>
A;Residuss: 1-1356 *FUS>
A;Residuss: 1-1356 *FUS>
A;Cross-references: UNIPROT:Q05546; UNIPARC:UPI00000E6D8A; GB:Z18630; NID:957961; PIDN:C?
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                                                                                                                                                                                                                                                                                                                                                                           C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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F;346-372/Domain: EGF homology <EGF>
F;377-403/Domain: EGF homology <EGF>
F;377-403/Domain: Edronectin type III repeat homology <FN3A>
F;711-793/Domain: fibronectin type III repeat homology <FN3B>
F;802-884/Domain: fibronectin type III repeat homology <FN3C>
F;892-976/Domain: fibronectin type III repeat homology <FN3C>
F;984-1064/Domain: fibronectin type III repeat homology <FN3E>
F;1073-1155/Domain: fibronectin type III repeat homology <FN3F>
F;164-1246/Domain: fibronectin type III repeat homology <FN3G>
F;1254-1335/Domain: fibronectin type III repeat homology <FN3G>
F;1343-1423/Domain: fibronectin type III repeat homology <FN3G>
F;1341-1511/Domain: fibronectin type III repeat homology <FN3G>
F;1841-1511/Domain: fibronectin type III repeat homology <FN3G>
F;1826-1334/Domain: fibronectin type III repeat homology <FN3G>
F;1826-1734/Domain: fibronectin type III repeat homology <FN3G>
F;1826-1734/Domain: fibronectin type III repeat homology <FN3G>
F;1826-1734/Domain: fibrinogen beta/gamma homology <FNGG>
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                                                                                                                                                                                                                                                                                                                          N; Alternate names: contactin; hexabrachion
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A; Residues: 1-772, 863-1356 <FU2>
                     744 EPGTEYTISIIA 755
                                                                                                                                                                                                                                                                                    tenascin precursor - pig
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                                                                                                                                                                             RESULT 10
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Estatus trefarences: UNIPROT: Q00546; UNIPARC: UPI00000FC0A7; GB: X64649; NID: g63613; PIDN: G
A; Experimental source: brain
A; Experimental source: brain
A; Accession: PS0385
A; Molecule type: protein
A; Residues: 579-586; 827-840 «NOE1-
A; Cross-references: UNIPARC: UPI0000174345
A; Cross-references: UNIPARC: UPI0000174345
C; Comment: This protein is a neural extracellular matrix protein implicated in neural of S; Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin type; C; Keywords calcium binding; cell adhesion; duplication; extracellular matrix; glycoprot F; 1-33/Domain: signal sequence #Etatus predicted <AIG>F: 34-1353/Product: restrictin #status predicted <AMT>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
Cross-treferences: UNIPROT:018977; UNIPARC:UPI00001101C4; EMBL:Y11915; NID:G2462978; PI
C;Genetics:
C;Genetics:
C;Genetics:
C;Supericmily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
C;Keywords: extracellular matrix; glycoprotein; heptad repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Gallus gallus (Chicken)
C;Species: Gallus gallus (Chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: 406675; F80385; S22284
R;Noerenberg, U; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
Neuron 8, 849-863, 1992
A;Title: The chicken neural extracellular matrix molecule restrictin: similarity with A;Reference number: JN6675; MUID:92265298; PMID:1375037
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; Pred. No. 0.00037;
13; Mismatches 28; Indels
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F)203-229/Domain: EGF homology <EG1>
F)234-260/Domain: EGF homology <EG2>
F)255-250/Domain: EGF homology <EG3>
F)256-321/Domain: EGF homology <EG3>
F)24-405/Domain: EGF homology <EG4>
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Matches 33; Conserv
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A; Map position: 6p21.3-6p21.3
C; Superfemily: BdF homology; fibringen beta/gamma homology; fibronectin type III repeat C; Superfamily: BdF homology; fibringen beta/gamma homology; fibronectin type III repeat homology astronectin typ
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Subscription of the protein protein precursor - rat

NyAlearnate names: leukocyte common antigen homolog

NyContains: protein-tyrosine-phosphatase (EC 3.1.3.48)

CyBecies: Rattus norvegicus (Norway rat)

CyAccession: 466216; 823122; A41032; A33154

RyZhang, W.R.; Hashimoto, W.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994

AyTitle: Nolecular cloning and expression of a unique receptor-like protein-tyrosine-pho
AyReference number: 546216; MUID:94347119; PMID:8068021

AyAccession: 546216 acid sequence not shown

AyAccession: 646216 acid sequence not shown

AyBecule type: mRNA

AyResidues: 1-1898 <ZHA>

AyCross-references: Uniprocy.064604; UNIPARC:UPI00000E87A8; EMBL:L11586; NID:g205132; PID

RyHabhimoto, N.; Zhang, W.R.; Goldstein, B.J.

Biochem. J. 284, 569-576, 1992

AyTitle: Insulin receptor and epidermal growth factor receptor dephosphorylation by thre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   748 VIDGPQDLRVVSVTPTTLELGWLRPQAEVDRFVVSY-VSADNQRVR-LEVPPETDGTLLT 805
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homology <3F27>
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                       A;Experimental source: clone 3.9kF3-1
A;Note: sequence extracted from NCBI backbone (NCBIP:95694)
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                                                                                                                                                        A;Gene: GDB:TNXA; D6S103B; TNX; XA; XB
A;Crose-references: GDB:568487; OMIM:600261
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Appearation: Molecular characterization and in situ mRNA localization of the neural residence number: $32023
A;Reference number: $32023
A;Actatus: Preliminary
A;Molecule type: mRNA
A;Residues: 1-1356 c/RUS2>
A;Reatus: Preliminary
A;Molecule type: mRNA
A;Residues: 1-1356 c/RUS2>
A;Residues: 1-136 c/RUS2>
A;Residues: 1-136
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A;Molecule type: DNA
A;Residues: 1-3566 -8RI>
A;Residues: 1-3566 -8RI>
A;Cross-references: UNIPROT: P22105; UNIPROT: Q9UC11; UNIPARC: UP10000174343; EMBL: X71937
A;Cross-references. J.; Gitelman, S.E.; Miller, W.L.
B;Morel, Y: Bristow, J.; Gitelman, S.E.; Miller, W.L.
A;Morel, Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/CA;Reference number: A33725; MUID: 89367293; PMID: 2475872
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A;Residues: 2748-3199, VV, 3201-3298, E', 3299-3314, G', 3316-3566 <MOR>
A;Cross-references: UNIPARC:UPI000016A98B; GB:M2S813; NID:g183069; PIDN:AAA35884.1; PID:
R;Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.
Genomics 12, 485-491, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Title: Cluster of fibronectin type III repeats found in the human major histocompatibi
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744 EPGAEYIISITAERGRQQSLESTVDAFTGFRPISHLHFSHV†SSSVNITWSDFSPPADRL 803
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C;Date: 10-Sep-1999 #text_change 31-Dec-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: A40701; A33725; C42175
R;Bristow, J; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.
J. Cell Biol. 122, 265-278, 1993
A;Title: Tenascin-X: a novel extracellular matrix protein encoded by the hur A;Reference number: A40701; MUID:99300909; PMID:7686164
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F;1133-1341/Domain: fibrinogen beta/gamma homology <FBG>
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; Pred. No. 0.0012;
18; Mismatches 3
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A;Residues: 1849-1936 <MAT>
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-2019 <SAGS.
A;Cross-references: UNIPROT:064706; UNIPARC:UPI000005D89C; GB:D90343; NID:G220609; PIDN:E
A;Experimental source: cell line 2H6GR
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: the authors translated the codon ATG for residue 60 as Trp
R;Weller, A.; Beck, S.; Ekblom, P.
J. Cell Biol. 112, 355-362, 1991
A;Title: Amino acid sequence of mouse tenascin and differential expression of two tenasco
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A,Molecule type: mRNA
A,Status: 1-201, E',203-317,'S',319-620,622-1010,'N',1012-1018,'S',1020-1024,'H',1026-3
A,Cross-references: UNIPARC:UP10000174346; GB:X56304
A,Crossion: B37936
A,Status: preliminary; nucleic acid sequence not shown
A,Molecule type: mRNA
A,Residues: 1-201,'E',203-317,'S',319-620,622-1010,'N',1012-1018,'S',1020-1024,'H',1026-3
A,Residues: 1-201,'E',203-317,'S',319-620,622-1010,'N',1012-1018,'S',1020-1024,'H',1026-3
A,Cross-references: UNIPARC:UP10000174347; GB:X56304
R,Weller, A.; Beck, S.; Ekblom, P.
Stwinted to the EMBL Data Library, August 1990
Submitted to the EMBL Data Library, August 1990
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A;Retus: preliminary
A;Acteus: preliminary
A;Retus: preliminary
A;Retus: preliminary
A;Retus: preliminary
A;Retus: preliminary
A;Retus: preliminary
A;Retus: preliminary
A;Residues: 1-201, E',203-317, S, 319-1018, S',1020-1024, H',1026-1305, S',1307-2019 kRE
A;Cross-references: UNIPARC:UPI00002A093; EMBL;X5304; NID:954768; PIDN:CAA39751.1; PID
R;Glumoff; V.; Savontaua, M.; Vehanen, J.; Vuorio, E.
Biochim: Biophys. Acta 1219, 613-622, 1994
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Reference number: S50206; MUID:9503091
A;Residues: de-lace number: S50206
A;Residues: de-lace number: S50206; MUID:95035091; PMID:7524681
A;Residues: de-lace number: S50206
A;Residues: de-lace number: S50206; MUID:9503091; PMID:7524681
A;Residues: de-lace number: S60209
A;Residues: de-lace number: de-lac
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A;Accession: $14571
          A;Title: Murine tenascin: cDNA cloning, structure and temporal expression of isoforms.
A;Reference number: JQ1322; MUID:92009211; PMID:1717349
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Pred. No. 0.0079;
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A; Accession: A37936
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                                                                                                                    A;Accession: JQ1322
A;Status: nucleic acid sequence not shown
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Matches 34; Conserv
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A;Reference number: S23126; MUID:92287069; PMID:1599438
A;Accession: S22252
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Residues: 1361-1604;1649-1898 «HAS»
A;Residues: 1361-1604;1649-1898 «HAS»
A;Cross-references: UNIPARC:UPI0000177056; UNIPARC:UPI0000177057
A;Cross-references: UNIPARC:UPI0000177056; UNIPARC:UPI0000177057
A;Cross-references: USBS-19696, 1991
A;Title: Cloning, bacterial expression, purification, and characterization of the cytopl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A33154
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1035-1072, 'S', 1074-1433, 'T',1435-1638,'N',1640-1642,'HT',1645-1898 <PO2>
A;Cross-references: UNIPARC:UPI00001709F3
C;Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatas
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: A41032
A,Molecule type: mRNA
A;Residues: 1035-1072, 'S',1074-1433,'T',1435-1638,'N',1640-1642,'HT',1645-1898 <POT>
A;Cross-references: UNIPARC:UPI00001709F3; GB:M60103; NID:g205130; PIDN:AAA41510.1; PID:
R;Pot, D.A.; Woodford, T.A.; Remboutsika, B.; Haun, R.S.; Dixon, J.E.
submitted to the Protein Sequence Database, December 1990
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N;Alternate names: contactin; hexabrachion
C;Species: Wus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: JQ1322; A37936; B37936; S14571; S50209
R;Saga, X.; Tsukamoto, T.; Jing, N.; Kusakabe, M.; Sakakura, T.
Gene 104, 177-185, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1539/Active site: Cys (phosphocysteine intermediate) #status predicted F;1545/Binding site: substrate phosphate (Arg) #status predicted F;1830/Active site: Cys (phosphocysteine intermediate) #status predicted F;1836/Binding site: substrate phosphate (Arg) #status predicted
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33; Conservative 1
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Cidence, 12. may 1990 #Requence_revision 21. may-1990 #text_Change 09-001-2004
Cidencesion: A1930
RiJones, F.S.; Burgoon, M.P.; Hoffman, S.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.M.
RiJones, F.S.; Burgoon, M.P.; Hoffman, S.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.M.
A; Matl. Acad. Sci. U.S.A. 85, 2186-2190, 1988
A; Title: A cDNA clone for cytocactin contains sequences similar to epidermal growth fact
A; Reference number: A31930; MUID:88176910; PMID:2451243
A; Residues: 1-933 a.ON>
A; Molecule type: mRNA
A; Residues: 1-931 a.ON>
A; Cross-references: UNIPROT:P10039; UNIPARC:UP1000177AF5
A; Octo: the authors' translation of the codons for residues 601-620 differs considerably
C; Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; FN335>
F; 134-215/Domain: EGF homology contains
F; 134-215/Domain: Edronectin type III repeat homology contains
F; 134-215/Domain: fibronectin type III repeat homology contains
F; 1499-576/Domain: fibronectin type III repeat homology contains
F; 1499-576/Domain: fibronectin type III repeat homology contains
F; 1495-576/Domain: fibronectin type III repeat homology contains
F; 1455-145/Domain: fibronectin type
RESULT 15
A31930
Cytotecin - chicken (fragments)
C;Species: Gallus gallus (chicken)
C;Species: Callway-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.9%; Score 108; DB 2; Length 933; Best Local Similarity 33.7%; Pred. No. 0.0052; Matches 32; Conservative 13; Mismatches 42; Indels
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Search completed: February 23, 2006, 07:48:17 Job time : 40 Becs

SGLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94

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3 DVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPW---ASIATI 59

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

OM protein - protein search, using sw model

February 23, 2006, 07:40:29 ; Search time 228 Seconds (without alignments) 290.876 Million cell updates/sec Run on:

US-09-688-566-81

494 1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKYDDPISINYRT Title: Perfect score: Sequence:

94

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Describcion	homod	рошо	homo	homo	рошо	homo	homo	homo	рошо	homo	homo	homo	homo	рошо	homo	рошо	bos t	P11276 mus musculu			orycto	Q91289 pleurodeles	Q91740 xenopus lae	Q6gga5 xenopus lae	Q4rnc4 tetraodon n	Q501r6 xenopus tro	_	Q6jan2 brachydanio		oryct	Q28377 equus cabal
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# ALIGNMENTS

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NARY; PRT; 787 AA. rel. 30, Created) rel. 30, Last sequence update) rel. 30, Last sequence) rel. 30, Last annotation update) r DKFZp68511370 (Fragment). Chordata; Craniata; Vertebrata; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Buarchontoglires; Primates; Catarrhini; Hominidae;	C., Sch i., Han i.tabases 	2; Length 787; -30; 17; Indels 0; Gaps TYGETGGNSPVQEFTVPGSKSTATIS	annotation update)
787 uence otatic Fragme Ea, Ve	line; , Rittmu ger A., enBank/L A. rog. GLU; UNK	361, D NO. 2.4 smatches GLOSRYYR :           AVTVRYYYR DPISINYR DPISINYR               KPISINYR :   1011	otatio
PRT; Created) Last seq Last seq SeI1370 (	rcinoma cell lin brium; 3. Regiert T., R Amid C., Boanger to the EMBL/GenB 7766.1; -; mRNA. Aldehyd dehydrog FNIII. FNIII. 8. 13. 14. 15. 16. 17. 18. 18. 19. 19. 19. 19. 19. 19. 19. 19	Score 361; D Pred: No. 2.4 4; Mismatches LISWNRSGLOSRYTR     :          :	Last
PRELIMINARY; PRT; 787 AA. (TrEMELrel. 30, Created) (TrEMELrel. 30, Last sequence upd protein DKPZp68611370 (Fragment) 211370. (Fragment) 511370. (Fragment) 51400n). etazoa; Chordata; Craniata; Vertecheria; Buarchontoglires; Primates06;	DE SEQUENCE.  And COMBORTIUM;  N. Krieger S., Regiert T., Rittmueller W., Weill B., Amid C., Osanger A., Fobo G.  N. FEB-2005) to the EMBL/GenBank/DDBJ die 1936633; CAL56766.1; -; mENAA.  PRO003086; Aldehyd dehydrog.  PRO003081; FN III Subd.  PRO0041; FN III.  PRO0041; FN IN III.  PRO0050; FN III.  PRO005	imilarity 77.7%; Pred. No. 2.4e; Conservative 4; Mismatches vsDvPRDLEVVAATPTSRLISWNRSGLOSRYYRI'SRAPROLEVVAATPTSLISWNRSGLOSRYYRI'SRAPROLEVVAATPTSLISWDAPATVRYYRYRYRYRYTTH	
IAN PRELIM  (TIEMBL )5 (TIEMBL )5 (TIEMBL )5 (TIEMBL )6 (TIEMBL )6 (TIEMBL )6 (TIEMBL )6 (TIEMBL )6 (TIEMBL )6 (TIEMBL )7	TIDE SEQUENCE.  "Budometrium Conservation Co	Similarity 3; Conser. VSDVPRDLE VIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	(Trem
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Query Match
Best Local Similarity 77.77
Matches 73; Conservative
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QEMZSO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Human colon endothel primary cell culture;
TISSUE-Human colon endothel primary cell culture;
The German Human cDNA Consortium;
The German Human cDNA Consortium;
The German Human cDNA Consortium;
A FODD G., Han M., Wiemann S.,
L Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; BX640638; CAE45786.1; -; mRNA.
SWR; Q6N044; 1-309, 402-601; -; mRNA.
SWR; Q6N044; 1-309, 402-601; -; mRNA.
R InterPro; IPR002086; Aldehyd dehydrog.
R InterPro; IPR003962; FMIII subd.
R InterPro; IPR003962; FNIII subd.
R InterPro; IPR003962; FNIII subd.
R FIREPRO; FF00039; FNIII Subd.
R FIREPRO; FF00039; FNIII Subd.
R FEAM; PF00041; FNIII.
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                                                                                                                                                                                                                          Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama Ohara O., Nagase T., Kikuno F.R.;
"None Tile.";
Submitted (Mak-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AB209287; BAD92524.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                    1011 AA; 110883 MW; 40CAF97C3023248D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686Lill144 (Fragment).
Name-DKFZp686Lill144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SMOODS8; FN1; 3.
SMART; SMOODS8; FN3; 8
PROSITE; PSOODS7; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
PROSITE; PSOOD22; EGF 1; UNKNOWN 1.
PROSITE; PSO1253; FIBKONECTIN 1; 3.
PROSITE; PS50853; FN3; 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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Fibronectin 1 variant (Fragment).
                       Name=Fibronectin 1 variant;
Homo sapiens (Human).
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PRINTS; PR00014; FNTYPEIII.
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Q6N084;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.7 tes 73; Conservative
                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                 NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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CON 084 HQ
CON 084 HQ
CON 084 HQ
CON 08-1
CON 08
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TISSUE-Human uterus endothel primary cell culture;
TISSUE-Human uterus endothel primary cell culture;
Tables J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
A Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Ann W. Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
BRBL: BX64020; CAR45558.1; -; mRNA.
BRIT: BX600039; 73-440, 531-624, 623-891.
BRITEPPO; IPR0003962; FAIII subd.
BRITEPPO; IPR0003962; FAIII subd.
BRITEPPO; IPR0003962; FAIII subd.
BRINTS; PR00013; FAITYPEI.
BRINTS; PR00014; FAITYPEII.
BRINTS; PR00014; FAITYPEII.
BRINTS; PR00015; FNITYPEII.
BRINTS; RN00058; FNI; 3.
BRART; SM00060; FNI; 3.
BROSITE; FS000627; EGF 1; UNKNOWN 1.
BROSITE; PS000227; EGF 1; UNKNOWN 1.
BROSITE; PS000227; EGF 1; UNKNOWN 1.
BROSITE; PS000227; FNITYPEIN 1; 3.
BROSITE; PS001253; FNIFONECTIN 1; 3.
BROSITE; PS01253; FNIFONECTIN 1; 3.
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                                                                                                                                                                                                                               216 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406
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                                                                                                                                                           1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS
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Score 361; DB 2; Length 1034;
Pred. No. 3.3e-30;
4; Mismatches 17; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1255 AA; 137247 MW; A8E454589E07FC07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686022169 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                               276 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 440
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Ottenwaelder B., Obermaler B., Deutschenbaur S., Schaipp A.,

Ottenwaelder B., Obermaler B., Deutschenbaur S., Schaipp A.,

Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (Aug-2004) to the EmBL/Genbank/DDBJ databases.

EMBL; CR749317; CAH18172.1; -; mRNA.

SMR; Q68DP8; 48-140, 305-464, 609-701, 1173-1540, 1633-1901.

Brsembl; RSKG0000011541; Homo sapiens.

R GO; G0:00015576; C:extracellular region; IEA.

GO; G0:0001576; C:extracellular region; IEA.

GO; G0:0001579; F:extendeductase activity; IEA.

GO; G0:000159; F:metabolism; IEA.

InterPro; IPR006209; EGF_like.

InterPro; IPR006309; EGF_like.

InterPro; IPR000309; FN III.

R InterPro; IPR000529; FN III.
                                                                                                                                                                                                                                                                                                                                1447 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSK&TATIS 1506
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                          1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                                                                                                                                                                                                            Query Match 73.1%; Score 361; DB 2; Length 2217; Best Local Similarity 77.7%; Pred. No. 8.3e-30; Matches 73; Conservative 4; Mismatches 17; Indels (
                                                                                           Wilson R.K.,
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2005) to the EMBL, AC012462; AAX76513.1; -; Genomic_DNA.
Hypothetical protein.
NON_TER 2217 2217
SEQUENCE 2217 AA; 243438 MW; FAFID07FBB6C44E5 CRC64;
                       Waterston R.;
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686H0342.
                                                                                                                                                                                                                                                                                                                                                                                                         1507 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 1540
                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2240 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodom; PD000995; FN Type_II; 2.
SMART; SM00059; FN1, 12.
SMART; SM00069; FN2; 2.
PRART; SW00060; FN3; 15.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
PROSITE; PS01022; EGF 1; 2.
PROSITE; PS01023; FN1_1; 10.
PROSITE; PS01021; FN1_2; 10.
PROSITE; PS01023; FN1_1; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
TISSUE-Amygdala;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0012; FNTYPEI.
PRINTS; PRO0013; FNTYPEII.
PRINTS; PRO0014; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEBDPB_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00039; fn1; 12.
Pfam; PF00040; fn2; 2.
Pfam; PF00041; fn3; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
NUCLEOTIDE SEQUENCE
                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=DKFZp686H0342;
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ID Q68DP8_F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.1%; Score 361; DB 2; Length 214 Best Local Similarity 77.7%; Pred. No. 8e-30; Matches 73; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2146 AA; 235425 MW; D526A8D713C571DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.H.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. [2]
             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical profession DKFZp686013149.
Name-DKFZp686013149;
Hypothetical Filman).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein FNI (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 2217 AA
                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
TISSUE=Colon endothel;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QS85T2_HUMAN PRELIMINARY;
QS85T2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 2146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=FN1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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RESULT (258572) (10 058572) (10 058572) (10 058572) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10 05872) (10

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NUCLEOTIDE SEQUENCE
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Matches
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                                                                                                                                                              1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kato S.;

Kato S.;

The man full-length cDNA starting with the capped site sequence.";

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

R Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB191261; BAD52437.1; "RNA.

R INTERPOSIONESTOR C: extracellular region; IEA.

R INTERPOSIONESTOR Aldehyd dehydrog.

R INTERPOSIONESTOR INTERPOSIONES
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                                                                                                  Score 361; DB 2; Length 2240;
Pred. No. 8.4e-30;
                                                                                                                                         4; Mismatches 17; Indels
PROSITE; PS51092; FN2_2; 2.
PROSITE; PS50853; FN3_15.
Hypothetical protein; Repeat.
SEQUENCE 2240 AA; 246668 MW; 8FCDAF406F330621 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2265 AA; 249411 MW; 74A67590564C28AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fram; FF00041; Fin3; 15.

PRINTS; PR00041; Fin3; 15.

PRINTS; PR00012; FNTYPEI.

PRINTS; PR00013; FNTYPEII.

PRODON; PR00014; FNTYPEIII.

Probon; PR00059; FN TYPEIII.

SMART; SM00059; FN TYPEIII.

SMART; SM00059; FN TYPEII.

SMART; SM00059; FN TYPEII.

PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.

PROSITE; PS01023; FIRRONECTIN 1; 12.

PROSITE; PS01023; FIRRONECTIN 2; 2.

PROSITE; PS50853; FN3; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                  1507 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 1540
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                                                                                                                                                                                                                                                                                                                                                                                                 2265 AA
                                                                                                  73.1%;
77.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                    24 HUMAN
QGOFE4 HUMAN PRELIMINARY;
QGOFE4;
                                                                           Query Match
Best Local Similarity 77...
Best Tocal Similarity 77...
73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=FN1;
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                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                               The German cDNA Consortium;

A Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,

Robbitted (ANG-2004) to the EMBL/GenBank/DDBJ databases.

B Submitted (ANG-2004) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005576; C:extracellular region; IEA.

R GO; GO:0008152; P:metabolism; IEA.

R InterPro; IPR000268; Aldehyd.dehydrog.

R InterPro; IPR000261; FPRIII.

R InterPro; IPR000562; FPRIII.

R InterPro; IPR000362; FNIII.

R InterPro; IPR000362; FNIII.

R Pfam; PP00040; fn2; 2.

R Pfam; PP00040; fn2; 2.

R Pfam; PR00013; FNIYEBII.

R PRINTS; PR00013; FNIYEBII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .l protein; Repeat.
2267 AA; 249359 MW; C4D124A038C323DF CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                  Last sequence update)
Last annotation update)
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  PRT; 2267 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; 1. PROSITE; PS01022; EGF 1; 2. PROSITE; PS01023; FN1 1; 12. PROSITE; PS01023; FN1 2; 12. PROSITE; PS01023; FN2 1; 2. PROSITE; PS01023; FN2 1; 2. PROSITE; PS05192; FN2 2; 2. PROSITE; PS05192; FN3 16. Hypothetical protein; Repeat.
                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
Hypothetical protein DKFZp686K08164.
Name=DKFZp686K08164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; PD000995; FW_TYPe_II; 2.
SMART; SM00058; FNI; 12.
SMART; SM00059; FN2; 2.
SMART; SM00060; FN3; 16.
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QGNOA6;
Q68DP9_HUMAN PRELIMINARY;
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ID QENOAE HU
AC QENOAE;
DT 05-JUL-20
DT 05-JUL-20
DT 05-JUL-20
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Gaps

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Length 2351;

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1533 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 1592
                                                                                                                                                                                                                1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS '60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
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R GO, GO:000576; C:extracellular region; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R InterPro; IPR0002086; Aldehyd dehydrog.

R InterPro; IPR0002086; Aldehyd dehydrog.

R InterPro; IPR000891; Fibrnctn1.

R InterPro; IPR000962; FN TIII.

R InterPro; IPR000391; FN III.

R InterPro; IPR000391; FN III.

R Pfam; PF00040; fn1; 12.

R Pfam; PF00041; fn3; 15.
                                                                                                                      73.1%; Score 361; DB 2; Length 23 77.7%; Pred. No. 8.9e-30; ive 4; Mismatches 17; Indels
                                                                         SEQUENCE 2351 AA; 258611 MW; 67149C626199075E CRC64;
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AB209840; BAD93077.1; -; mRNA. NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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PRINTS; PRO0013; FNTYPEI.
PRINTS; PRO0014; FNTYPEII.
PRINTS; PRO0014; FNTYPEII.
ProDom; PD000995; FNTYPEIII.
SMART; SM00059; FNZ; 2.
SMART; SM00069; FNZ; 2.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
PROSITE; PS01253; FNI_1; 12.
PROSITE; PS01253; FNI_1; 12.
PROSITE; PS01253; FNI_1; 12.
PROSITE; PS01253; FNI_1; 12.
PROSITE; PS01091; FNI_2; 12.
PROSITE; PS01091; FNI_2; 12.
PROSITE; PS01091; FNI_2; 2.
PROSITE; PS01091; FNI_2; 2.
PROSITE; PS01091; FNI_2; 2.
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2357 AA; 259092 N
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The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q68DT4 HUMAN
ID Q68DT4 HUMAN PRELIMINARY;
AC Q68DT4;
                                                                                                                                            Best Local Similarity 77.74
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=DKFZp686F10164;
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SEQUENCE 23
                                                                                                                           Query Match
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                           Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagage T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                      Bloecker H., Seecher M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BX640608; CAS45714.1; -; mRNA.
EMBL, BX640608; CRExtracellular region; IRA.
InterPro; IPR002096; Aldehyd_dehydrog.
InterPro; IPR003093; Fibrnctnl.
InterPro; IPR003962; FnIII. subd.
InterPro; IPR003962; FNIII.
InterPro; IPR003662; FNIII.
InterPro; IPR003662; FNIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 2296 AA; 252761 MW; 9AB2D723CCOCED70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRODUCT; ENTYPEII.
PRINTS; PRODUCT; ENTYPEII.
PRINTS; PRODUCT; ENTYPEII.
PRINTS; PRODUCT; ENTYPEII.
PRODUCT; PRODUCCT; ENTYPEIII.
PRODUCT; SMOODS; FNI; 12.
SMART; SMOODS; FNI; 12.
SMART; SMOODS; FNI; 15.
SMART; SMOODS; FNI; 15.
PROSITE; PSOOGS; FNI; 15.
PROSITE; PSOOCS; BCT I, UNKNOWN 2.
PROSITE; PSOOLS; BCT I, UNKNOWN 2.
PROSITE; PSOOLS; BCT I, UNKNOWN 2.
PROSITE; PSOOLS; FNI; 15.
PROSITE; PSOORS; FNI; 15.
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Q59EH1;
10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
         Hypothetical protein DKF2p686M04163.
Name=DKF2p686M04163;
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                                                                                                                                                                                                                   TISSUE=Uterus endothel;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Fibronectin 1 variant;
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nes 73; Conservative
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Pfam; PF00040; fn2; 2.
Pfam; PF00041; fn3; 15.
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                                                        Homo sapiens (Human)
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RESULT 11
0259EHL HUM
10 0559EH
AC 059EH
DT 10-MA
DT 11-MA
DT 11-M

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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLECTIDE SEQUENCE OF 1-49.
MEDLINE=87175578; PubMed=3031656;
Dean D.C., Bowlus C.L., Bourgeois S.;
"Cloning and analysis of the promotor region of the human fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 103-481; 1116-1422 AND 2228-2386 (ISOFORM 1), NUCLEOTIDE SEQUENCE OF 1919-2161 (ISOFORMS 3/7), NUCLEOTIDE SEQUENCE OF 1449-1825 (ISOFORMS 8/9/10), NUCLEOTIDE SEQUENCE OF 1233-2160 (ISOFORM 9), AND NUCLEOTIDE SEQUENCE OF 1238-2160 (ISOFORM 12). TISSUB-Peripheral blood T-cell, and Umbilical vein endothelial cell; Godfrey H.P., Ebrahim A.A.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Primary structure of a DNA- and heparin-binding domain (Domain III) in human plasma fibronectin."; J. Biol. Chem. 260:12136-12141(1985).
                                                                                                                                                                                                                                                                                                                        MEDLINE-21600194; PubMed=11737888; DOI=10.1186/bcr325;
Schor S.L., Schor A.M.;
"Phenotypic and genetic alterations in mammary stroma: implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 1-38.
MEDLINE=87030890; PubMed=3770189; DOI=10.1016/0014-5793(86)80029-1; Gutman A., Yamada K.M., Kornblihtt A.R.; Human fibronectin is synthesized as a pre-propolypeptide."; FEBS Lett. 207:145-148(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85284965; PubMed=2992939;
Kornblihtt A.R., Umezawa K., Vibe-Pedersen K., Baralle F.B.;
"Primary structure of human fibronectin: differential splicing may
generate at least 10 polypeptides from a single gene.";
EMBO J. 4:1755-1759(1985).
                                                                                                                                                QGLDP6; Q86T27;
Q9UMK2;
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MEDLINE-86008277; PubMed=1900070;
Calaycay J., Pande H., Lee T., Borsi L., Siri A., Shively J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 3; 7 AND 10)
                                                                                                                                                                                                annotation update)
(Cold-insoluble globulin) (CIG)
                                                                                                                                                                                                                                                                                                                                                                                                                           The German cDNA consortium;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).
                                                             FINC. HUMAN STANDARD; PRT; 2386 AA. P02751; O95609; O95610; Q14312; Q14325; Q14325; Q18118; Q96KP1; Q96KP9; Q96KP9; Q911B8; Q91AP3; 21-JUL-1986 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Pibronectin precursor (FN) (Cold-insoluble globu
                                                 94
                                                 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE OF 28-2386 (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                           Breast Cancer Res. 3:373-379(2001)
                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                 for tumour progression.";
                                                                                                                                                                                                                           Name=FN1; Synonyms=FN;
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PROTEIN SEQUENCE OF 1441-1548.
MEDLINE=82256564; PubMed=7050098;
Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
"The cell attachment domain of fibronectin. Determination of the
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MEDLINES-87241275; PubMed=3593230;
Garcia-Pardo A., Rostagno A., Frangione B.;
"Primary structure of human plasma fibronectin. Characterization of a "Primary structure of human plasma fibronectin. Characterization of a 18 kDa domain containing the C-terminal heparin-binding site (Hep III site) and a region of molecular heterogeneity.";
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"Sequence analysis and in vivo expression show that alternative
splicing of ED-B and ED-A regions of the human fibronectin gene are
independent events.";
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Kornblihtt A.R., Vibe-Pedersen K., Baralle F.E.;
"Human fibronectin: molecular cloning evidence for two mRNA species
differing by an internal segment coding for a structural domain.";
EMBO J. 3:221-226(1984).
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NUCLEOTIDE SEQUENCE OF 973-2386 (ISOPORM 3).
MEDLINE=84272258; PubMed=6462919;
MCDLINE=84272258; Vibe-Pedersen K., Baralle F.E.;
"Human fibronectin: cell specific alternative mRNA splicing genera
"Human fibronectin: cell specific alternative mRNA splicing genera
polypeptide chains differing in the number of internal repeats.";
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MEDLINE=88029324; PubMed=2812387;
Zardi L., Carnemolla B., Siri A., Petersen T.E., Paolella G.,
Sebastio G., Baralle F.E.;
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Haman cellular fibronectin: comparison of the portion with rat identifies primary structural
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MEDLINE=880401707, PUNMCd=3478690;
MEDLINE=880401707, PUNMCd=3478690;
MEDLINE=880401707, PUNMCd=3478690;
"Identification of a third region of cell-spec
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J. Biol. Chem. 257:9593-9597(1982)
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MEDLINE=86111901; Pubmed=3003095;
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Biochemistry 24:2698-2704(1985).
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Sebastio G., E
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EMBO J. 5:2825-2830(1986).
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"Tyrosine sulfation of proteins from the human hepatoma cell line
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MEDLINE-22126816; PubMed=12127832; DOI=10.1053/joca.2002.0792;
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                                            MEDLINE=87026578; PubMed=3021206;
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PubMed=6304699;
                      NUCLEOTIDE SEQUENCE OF 1712-1739
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Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
B. Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
B. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
B. Mach. Bx640731; CAE45847.1; — RRNA.
B. GO; GO:005576; C:extracellular region; IEA.
B. InterPro; IPR002066; Aldehyd_dehydrog.
B. InterPro; IPR002065; Fibrictal.
B. InterPro; IPR00095; Fibrictal.
B. InterPro; IPR00095; Fibrictal.
B. InterPro; IPR00095; FNIII subd.
B. InterPro; IPR000952; FNIII subd.
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SMART; SM00059; FN1; 12.
SMART; SM00069; FN2; 2.
SMART; SM00060; FN2; 16.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNIPROSITE; PS01022; EGF I; UNKNOWN Z.
PROSITE; PS01023; FIBRONECTIN_1; 12.
PROSITE; PS00023; FIBRONECTIN_2; 2.
PROSITE; PS00833; FIBRONECTIN_2; 2.
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                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                         TNOCLEDING SUCCESSION OF THE SECONDARY OF THE GERMAN CARCINOMA CONSORTIUM;

TASSUE-Endometrium carcinoma cell line;

The German cDNA Consortium;

A Bloecker H., Breacher M., Brandt P., Mewes H.W., Weil B., Amid C.,

B Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, BX640875; Carkracellular region; IEA.

R InterPro; IPR002086; Aldehyd dehydrog.

R InterPro; IPR000088; Pibrnchil.

R InterPro; IPR001961; Pibrnchil.

R InterPro; IPR001961; FN III.

R InterPro; IPR001961; FN III.

R Pfam; PF00019; fil.; 12.

R Pfam; PF00040; fil.; 2.

R Pfam; PF00041; fil.; 2.

R Pfam; PF00041; fil.; 2.
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PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
PROSITE; PS0022; EGF 1, UNKNOWN 2.
PROSITE; PS0153; FIBRONECTIN_1; 12.
PROSITE; PS00023; FIBRONECTIN_2; 2.
PROSITE; PS50853; FN3; 17.
Hypothetical protein.
SEQUENCE 2477 AA; 272335 MW; D358D85C6B18207C CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                Hypothetical protein DKFZp68601166.
Name=DKFZp68601166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00012; FNTYPEI.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00014; FNTYPEIII.
ProDom; PD000995; FN Type_II; 2.
SNART; SM00089; FN1; 12.
SNART; SM00089; FN1; 12.
                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                              NCBI_TaxID=9606;
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Search completed: February 23, 2006, 07:47:33 Job time : 230 secs

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1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKYDDPISINYRT 94
GenCore version 5.1.7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

geneseqp20018:

geneseqp2005s:*

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*

Genesed

Database

Abb78898 Tumour ne Abb78921 Tumour ne Abb78929 Tumour ne Abb78919 Tumour ne Abb78919 Tumour ne Abb78911 Tumour ne Abb78915 Tumour ne Abb78915 Tumour ne Abb78912 Tumour ne Abb78912 Tumour ne Abb78913 Tumour ne Abb78913 Tumour ne Abb78913 Tumour ne Abb78913 Tumour ne Abb78923 Tumour ne Abb78931 Tumour ne Tumour Tumour Tumour Tumour Tumour Description Abb78942 7 Abb78870 7 Abb78900 7 Abb78871 7 SUMMARIES ABB78940 ABB78912 ABB78916 ABB78918 ABB78899 ABB78917 ABB78949 ABB78873 ABB78869 ABB78870 ABB78900 ABB78871 ABB78872 ABB78942 ABB78915 ABB78922 ABB78868 ABB78911 В Query Match Length 443 439 437.5 437 Score 431 419 417 416 416 Result

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25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

RESULT 1

Tumour necrosis factor-alpha binding amino acid sequence T10.06. Protein scaffold, antibody, binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework. Kuimelis RG; ABB78898 standard; peptide; 94 AA 16-OCT-2000; 2000US-00688566 16-OCT-2001; 2001WO-US032233 (first entry) Wagner RW, WPI; 2002-444238/47. (PHYL-) PHYLOS INC WO200232925-A2 Lipovsek D, 30-JUL-2002 25-APR-2002 Synthetic. ABB78898; 

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest.

Claim 47; Fig 25; 94pp; English.

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel

proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Bacherichia coli), in eukaryotic systems (e.g. Pacherichia coli), in eukaryotic systems (e.g. veast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in binding proteins useful in the above-mentioned fields. The present exemplification of the present invention the 8X8888888888888X8

Sequence 94 AA;

ö 9 9 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGRTGGNSPVQEFTVPPWASIATIS Gaps ; 0 100.0%; Score 494; DB 5; Length 94; 100.0%; Pred. No. 1.2e-49; Indels ö 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 0; Mismatches 94; Conservative Best Local Similarity 61 Query Match Matches 셤 ò 8

RESULT 2 ABB78921

ABB78921 standard; peptide; 94 AA

(first entry) 30-JUL-2002 ABB78921;

Tumour necrosis factor-alpha binding amino acid sequence T14.26.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework. 

Homo sapiens

Synthetic.

25-APR-2002

WO200232925-A2

16-OCT-2001; 2001WO-US032233

16-OCT-2000; 2000US-00688566

(PHYL-) PHYLOS INC.

Kuimelis RG; Wagner RW, Lipovsek D,

WPI; 2002-444238/47.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen

Claim 47; Fig 25; 94pp; English.

domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of The present invention describes a non-antibody protein, comprising

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is

Claim 47; Fig 25; 94pp; English.

interest, or for destroying or inactivating antibody molecules. The nonantibody protein is also useful in all areas where antibodies are used,
e.g. research, therapeutic or diagnostic fields, and for screening novel
binding proteins useful in the above-mentioned fields. The present
proteins have thermodynamic properties superior to those of natural
antibodies, and can be evolved rapidly in vitro. The present proteins or
antibody mimics exhibit improved biophysical properties, such as
stability under reducing conditions and solubility at high
concentrations. In addition, these molecules are readily expressed and
concentrations. In addition, these molecules are readily expressed and
concentrations. In addition, these molecules are exacting
folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
reticulocyte lysate system). Furthermore, these proteins are extremely
amenable to affinity maturation techniques involving multiple cycles of
selection, e.g. in vitro selection using RNA-protein fusion technology,
phage display or yeast display systems. The present sequence is used in
the exemplification of the present invention ö New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest. 9 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS Gaps Numour necrosis factor-alpha binding amino acid sequence M12.01. ö Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework. Length 94; Indels ; Score 494; DB 5; ; Pred. No. 1.2e-49; 0; Mismatches 0; GLKPGVDYTITVYAVTDKSDTYKYDDFISINYRT 94 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 Kuimelis RG; ABB78939 standard; peptide; 94 AA. 100.0%; 16-OCT-2001; 2001WO-US032233. 16-OCT-2000; 2000US-00688566 (first entry) 94; Conservative Wagner RW, WPI; 2002-444238/47. Similarity (PHYL-) PHYLOS INC. Sequence 94 AA; WO200232925-A2. sapiens. Lipovsek D, 30-JUL-2002 25-APR-2002 Synthetic. ABB78939; Query Match Best Local 8 Matches RESULT 3 ABB78939 g ઠ 셤 ઠે

is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. peast), or in in vitro translation systems (e.g. rabbit efficity maturation techniques involving multiple cycles of smenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention 

Sequence 94 AA;

ö VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS ö Score 489; DB 5; Length 94; Pred. No. 4.4e-49; 2; Mismatches 0; Indels GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 GLKPGVDYTITVYAVTDESDTYKYDDPVSINYRT 94 99.0%; Local Similarity 97.9 es 92; Conservative 19 Query Match Matches ద 8 g 8

ABB78919 standard; peptide; 94 AA ABB78919;

(first entry) 30-JUL-2002 Numour necrosis factor-alpha binding amino acid sequence T14.14.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens Synthetic. WO200232925-A2

25-APR-2002.

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566

(PHYL-) PHYLOS INC.

Kuimelis RG; Wagner RW, Lipovsek D,

WPI; 2002-444238/47.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen ABB78919
ABB

Claim 47; Fig 25; 94pp; English.

The present invention describes a non-antibody protein, comprising

protein having a mutated amino acid sequence, where the non-antibody protein hinds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present Intuining proteins useful. In the above mentioned trade, the present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Bscherichia coli), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the present invention the exemplification of

Sequence 94 AA;

Gaps ö Length 94; Indels 99.0%; Score 489; DB 5; 98.9%; Pred. No. 4.4e-49; iive 0; Mismatches 1. 93; Conservative Local Similarity Query Match Matches

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61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 GLKPGVDYTITVYAVTDKSDTYKYDDPTSINYRT 94

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ABB78920 standard; peptide; 94 AA

ABB78920; 

30-JUL-2002 (first entry)

Tumour necrosis factor-alpha binding amino acid sequence T14.23.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens.

Synthetic

WO200232925-A2

25-APR-2002

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566

(PHYL-) PHYLOS INC.

Kuimelis RG; Lipovsek D, Wagner RW,

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Claim 47; Fig 25; 94pp; English.
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New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for

Kuimelis RG;

Lipovsek D, Wagner RW, WPI; 2002-444238/47.

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designing proteins with specific properties, e.g. for binding any antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQELTVPPWASIATIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                                                                                   The present invention describes a non-antibody protein, comprising domain having an immunoglobulin-like fold, derived from a reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Numour necrosis factor-alpha binding amino acid sequence T14.12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.9%; Score 488; DB 5; 98.9%; Pred. No. 5.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB78915 standard; peptide; 94 AA.
                                                          Claim 47; Fig 25; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001; 2001WO-US032233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 98.9 es 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 94 AA;
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                       of interest
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Matches
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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is acaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, threspeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins useful in the above-mentioned fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing condition, these molecules are readily expressed and concentrations. In addition, these molecules are readily expressed and concentrations. In addition, these molecules are readily expressed and colded in prokaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system) Furthermore, these proteins are extremely amended to a ffinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen Claim 47; Fig 25; 94pp; English.

Sequence 94 AA;

ö 9 9 VSDVPRDLEVVAATPTSRLISWNRSGLOSRYYRITYGETGGNSPVOEFTVPPWASIATIS 1 LSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIAAIS 0; Gaps DB 5; Length 94; 1; Indels GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 Score 486; DB 5; Pred. No. 1e-48; 1; Mismatches 98.4%; 97.9%; Query Match
Best Local Similarity 97.5.
Best Local Similarity 97.5.
Best Local Similarity ઠે 셤 8 a

ABB78940 RESULT

ABB78940 standard; peptide; 94 AA (first entry) 30-JUL-2002 ABB78940; 

Tumour necrosis factor-alpha binding amino acid sequence M12.01.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNP-alpha; protein framework.

Homo sapiens Synthetic.

WO200232925-A2

25-APR-2002.

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566.

(PHYL-) PHYLOS INC.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigne of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins or proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solublity at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Bscherichia coll), in eukaryotic systems (e.g. pscherichia coll), in eukaryotic systems (e.g. pscherichia coll), in eukaryotic systems (e.g. reabit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention Kuimelis RG; Claim 47; Fig 25; 94pp; English. Wagner RW, WPI; 2002-444238/47. Lipovsek D, of interest 

Sequence 94 AA;

9 1 VSDVPRDLEVVAATPISRLISWNRSGLOSRYYRITYGETGGNSPVQEFTVPPWASIATIS Gaps ; 0 Length 94; Indels Match 98.0%; Score 484; DB 5; Local Similarity 96.8%; Pred. No. 1.7e-48; les 91; Conservative 2; Mismatches 1; Query Match Best Loc Matches

61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 GLKPGVDYTITVYAVTDESDTYKYDDPVSTNYRT 94

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RESULT 9 ABB78912 ABB78912 standard; peptide; 94 AA ABB78912; 

30-JUL-2002 (first entry)

Tumour necrosis factor-alpha binding amino acid sequence SO8.03.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens. Synthetic.

WO200232925-A2

25-APR-2002

16-OCT-2001; 2001WO-US032233

16-OCT-2000; 2000US-00688566

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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mW to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fleads, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibody minics exhibit improved biophysical properties, such as attibody minics exhibit improved biophysical properties, such as attibody minics exhibit improved biophysical properties, such as attibody minics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and colded in prokaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                        New non-antibody proteins having an immunoglobulin fold, useful in
research, therapeutic or diagnostic fields, particularly as scaffolds for
dealgning proteins with specific properties, e.g. for binding any antigen
of interest.
                                                                                                                                                                                                                                                                                                                                  Claim 47; Fig 25; 94pp; English
                                                                                Lipovsek D, Wagner RW,
                                                                                                                                 WPI; 2002-444238/47
                         (PHYL-) PHYLOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 94 AA;
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9 9 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 1 VSDVPRDLEVVAATPTSRLISWNRSGLOSRYYRITYGETGGNGPVQEPTVPPWASIATIS Gaps ó, 98.0%; Score 484; DB 5; Length 94; 97.9%; Pred. No. 1.7e-48; ive 0; Mismatches 2; Indels 61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 61 GLKPGVDYTITVYAVTDMSDTYKYDDPISINYRT 94 92; Conservative 셤 Š

RESULT 10

ABB78916 standard; peptide; 94 AA 

30-JUL-2002 (first entry)

ABB78916;

Tumour necrosis factor-alpha binding amino acid sequence T14.13.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens Synthetic. WO200232925-A2

25-APR-2002,

16-OCT-2001; 2001WO-US032233 \$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac

16-OCT-2000; 2000US-00688566

(PHYL-) PHYLOS INC

Kuimelis RG;

Kuimelis RG; Wagner RW, Lipovsek D,

WPI; 2002-444238/47.

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest

Claim 47; Fig 25; 94pp; English.

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference of protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibody mimics exhibit improved hophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and contactions. folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention

Sequence 94 AA;

Gaps ö Length 94; Indels 97.8%; Score 483; DB 5; 97.9%; Pred. No. 2.2e-48; 1; Mismatches Best Local Similarity 97.9 Matches 92; Conservative Query Match

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RESULT 11 ABB78918

ABB78918 standard; peptide; 94 AA.

ABB78918;

(first entry) 30-JUL-2002 Tumour necrosis factor-alpha binding amino acid sequence T14.05.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

sapiens. Synthetic BXSSXXXXXXXXXXXXX

WO200232925-A2

Kuimelis RG;

Lipovsek D, Wagner RW, WPI; 2002-444238/47

(PHYL-) PHYLOS INC.

16-OCT-2001; 2001WO-US032233 16-OCT-2000; 2000US-00688566

WO200232925-A2.

Synthetic.

25-APR-2002

us-09-688-566-81.rag

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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mW to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins useful in the above-mentioned fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and colded in prokaryotic systems (e.g. reads). Or in in vitro translation systems (e.g. rabbit reticulocyte lysate systems). Furthermore, these proteins are extremely membrale to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, bagge display or yeast display systems. The present sequence is used in
                                                                                                                                                                                                                                                                                                               New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen
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                                                                                                                                                                                                                   Kuimelis RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 47; Fig 25; 94pp; English
                                                                       16-OCT-2001; 2001WO-US032233.
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                                                                                                                                                                                                                   Wagner RW,
                                                                                                                                                                                                                                                                 WPI; 2002-444238/47
                                                                                                                                                                     (PHYL-) PHYLOS INC.
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                         25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                            of interest
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1 VSDVPRDLEVVAATPISRLISWNRSGLQSRYYRIIYGETEGNSPVQEFTVPPWASMATIS
                                                                VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
                                       Gaps
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                                     1; Indels
           97.8%; Score 483; DB 5;
97.9%; Pred. No. 2.2e-48;
tive 1; Mismatches 1;
                                                                                                                    94
                                                                                                                                  61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT
Query Match
Best Local Similarity 97.9'
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Tumour necrosis factor-alpha binding amino acid sequence T10.17.
                 ABB78899 standard; peptide; 94 AA
                                                   (first entry)
                                                    30-JUL-2002
                                 ABB78899;
RESULT 12
ABB78899
                SXXXXXXXXXXXXXX
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**XXXXXXXXX** 

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

ношо варіепв

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New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigne of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia coll), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely smenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 481; DB 5;
Pred. No. 3.8e-48;
0; Mismatches 1
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the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 47; Fig 25; 94pp; English
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Best Local Similarity
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Tumour necrosis factor-alpha binding amino acid sequence T14.24

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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutaced amino acid sequence, where the non-antibody protein binds with a feat as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and
                                                                                                                                                                                                                                                                                                                                                                                                                  New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, phage display or yeast display systems. The present sequence is used in the exemplification of the present invention
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tumour necrosis factor alpha; TNF-alpha; protein framework.
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                                                                                                                                                                                                                                                                                                                              Kuimelis RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 47; Fig 25; 94pp; English
                                                                                                                                                                                              16-OCT-2001; 2001WO-US032233
                                                                                                                                                                                                                                          16-OCT-2000; 2000US-00688566
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                                                                                                                                                                                                                                                                                                                              Lipovsek D, Wagner RW,
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                                                                                                                                                                                                                                                                                     (PHYL-) PHYLOS INC.
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                                                                                                          WO200232925-A2
                                             Homo sapiens
                                                                                                                                                     25-APR-2002
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                                                                    Synthetic
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ABB78923 standard; peptide; 94 AA.
                     Query Match
Best Local Similarity
Matches 88; Conserv
Sequence 94 AA;
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ABB78923
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                                                         VSDVPRGLEVVAATPISRLISWNRSGLQSRYYRITYGRIGGNSPVQEFTVPPWASIATIS 60
                                                                                                                                                                                        ABB78922 standard; peptide; 94 AA
                                                                                                                                                                                                                                              (first entry)
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RESULT 14

ABB78922 ID ABB7 XX AC ABB7 XX DT 30-J

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The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein blinds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as caffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibody mimics exhibit improved biophysical properties, such as antibodies, and can be evolved rapidly in vitro. The present proteins or stability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and folded in prokaryotic systems (e.g. Escherichia coll), in eukaryotic systems (e.g. Escherichia ere extremely reticulocyte lysate system). Furthermore, these proteins are extremely amended to affinity maturation techniques involving multiple cycles of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen
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                                       Protein scaffold, antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.
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Pred. No. 4.9e-46;
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                                                                                                                                                                                                                                                                                                         16-OCT-2000; 2000US-00688566.
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1 Similarity 93.6%;
88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-444238/47
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                                                                                                                                                                        WO200232925-A2
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                                                                                                                              Synthetic
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(first entry)
30-JUL-2002
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Tumour necrosis factor-alpha binding amino acid sequence T14.20.

Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.

Homo sapiens

Synthetic.

WO200232925-A2.

25-APR-2002

16-OCT-2001; 2001WO-US032233.

16-OCT-2000; 2000US-00688566.

(PHYL-) PHYLOS INC.

Kuimelis RG; Lipovsek D, Wagner RW,

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest.

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel pinding proteins useful in the above-mentioned fields. The present proteins have thermodynamic properties superior to those of natural antibodies, and can be evolved rapidly in vitro. The present proteins or extability under reducing conditions and solubility at high concentrations. In addition, these molecules are readily expressed and concentrations. In addition, these molecules are readily expressed and solubility and extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection user stremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection the present sequence is used in the exemplification of the present invention

0; Gaps 90.3%; Score 446; DB 5; Length 94; 91.5%; Pred. No. 4.8e-44; rive 1; Mismatches 7; Indels Local Similarity 91.5 nes 86; Conservative Query Match Best Loca Matches

1 VSDVPRDLEVVAATPISRLISWRNIYPIARYYRITYGETGGNSPVQEFTVPPWASIATIS

94 

Search completed: February 23, 2006, 07:43:38 Job time : 187 secs

WPI; 2002-444238/47

Claim 47; Fig 25; 94pp; English.

Sequence 94 AA;

1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60

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GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94 61

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110, App
8, Appli
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Sequence 110, App
Sequence 112, App
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                                                                                   ; Search time 47 Seconds (without alignments)
165.351 Million cell updates/sec
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1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKYDDPISINYRT
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-538-202A-110
US-09-528-901A-8
US-09-638-202A-110
US-09-638-202A-112
US-09-638-202A-112
US-09-638-202A-112
US-09-638-202A-112
US-09-637-614-112
US-09-723-718-34
US-09-723-718-34
US-09-723-69-11
US-07-959-369-10
US-07-959-369-11
US-07-959-369-11
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US-08-809-156B-29
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                                                                                                                                                                                                                                                     572060 segs, 82675679 residues
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                                                                                     February 23, 2006, 07:47:49
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Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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302 2 US-09-775-964-29 332 1 US-08-836-854-13 341 1 US-08-836-854-14 368 1 US-08-836-854-18 368 1 US-08-836-854-18 383 1 US-07-959-369-5 385 1 US-07-959-369-14 422 1 US-08-836-854-10 432 1 US-07-959-369-9 432 1 US-07-959-369-9 432 1 US-07-959-369-9 432 1 US-07-959-369-9 432 2 US-09-366-854-20 433 2 US-09-156B-4 446 1 US-08-836-854-16 446 1 US-08-836-854-16 447 1 US-08-836-854-16	Sequence 29, Appl Sequence 13, Appl Sequence 14, Appl	10, 41, 10, 10, 10, 10, 10, 10, 10, 10, 10, 1	Sequence 8, Appli Sequence 9, Appli Sequence 9, Appli Sequence 20, Appl Sequence 4, Appli Sequence 4, Appli	Sequence 4, Appli Sequence 15, Appli Sequence 16, Appl Sequence 5, Appli
2749333355235 27493333552325 27493333552325 274933335525 2749355	US-09-775-964-29 US-08-836-854-13 US-08-836-854-14	US-08-836-854-10 US-08-836-854-17 US-07-959-369-5 US-08-836-884-10	US-08-836-936-91 US-07-959-369-8 US-07-959-369-9 US-08-836-854-20 US-09-366-009-4 US-08-809-156R-4	US-09-775-964-4 US-08-836-854-15 US-08-836-854-16 US-09-366-009-5
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# ALIGNMENTS

Sequence 8, Application US/08717169
Patent No. 592576
GENERAL INFORMATION:
MAPLICANT: Rucalalti, Renata
APPLICANT: Rucalalti, Rerki
TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
TITLE OF INVENTION: Angiotect 12
COMPUTER: 1370 La Joula Village Drive, Suite 700
STATE: Californal Angiotect 12
COMPUTER: Tabababe FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Batenin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/717,169
FILING DATE: 20-SE1-1996
CLASSIFICATION NUMBER: 13,135
ATTORNEY/AGENT INPORMATION:
MAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 13,135
ATTORNEY/AGENT INPORMATION:
TELEPOWHUNICATION INPORMATION:

8 8

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Diskette
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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CRIGINAL SOURCE:
US-09-096-749A-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-228-901A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
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73.1%; Score 361; DB 2; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.8e-35;
Matches 73; Conservative 4; Mismatches 17; Indels
                                                                                                                                                           RESULT 2
US-09-638-202A-110
; Sequence 110, Application US/09638202A
; Patent No. 6462B9;
; GENERAL INFORMATION:
APPLICANT: Koieda, Shohe;
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
· CORRESPONDENCE ADDRESS:
· CORRESPONDENCE ADDRESS:
· CORRESPONDENCE ADDRESS:
· TITLE OF INVENTION: ANDRESS:
· CORRESPONDENCE ADDRESS:
· TITLE OF INVENTION: ANDRESS:
· CORRESPONDENCE ADDRESS:
· TITLE OF INVENTION: ANDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/096,749
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikenins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,202A
FILING DATE: 11-Aug-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
RAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-638-202A-110
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1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
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TITLE OF INVENTION: Ameliorating Cancer by Using Superfibronectin FILE REFERENCE: P-TX 3416
CURRENT APPLICATION NUMBER: US/09/228,901A
CURRENT FILING DATE: 200-05-10
PRIOR APPLICATION NUMBER: US 08/717,169
PRIOR FILING DATE: 1996-09-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-096-749A-110

Sequence 110, Application US/09096749A

Patent No. 6673901

GENERAL INFORMATION:
APPLICANT: Koieda, Shohei

TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                Score 361; DB 2;
Pred. No. 1.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: DOS SOFTWARE: DOS SOFTWARE: PASTSEQ Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/096,749A PILING DATE: June 12, 1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING NAME: FILING NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. VİKSINIS
REGISTRATION NUMBER: 37,748
REFRENCE/DOCKET NUMBER: 109.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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RESULT
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                                                                                                      1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                                                              1 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 60
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                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                              Sequence 110. Application US/09637614
Patent No. 6703199
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Koided, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
                   Score 361; DB 2; Length 94;
Pred. No. 1.8e-35;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 94;
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                                                                                                                                                                                       61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                               GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/096,749
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikenins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/637,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-Aug-2000 PRIOR APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                     73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
Query Match
Best Local Similarity 77...
Best Local Similarity 77...
Annual Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 55402
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                             RESULT 5
US-09-637-614-110
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1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
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                                                                                                                                                                               ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
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; Sequence 112, Application US/09096749A
; Patent No. 6673901
; PAPLICANT: Koieda, Shohei
; TITLE OF INVENTION:
; TITLE OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; STREET: ADDRESSEE SCHWEGMAN, Lundberg, Woesener & Kluth P.A.
; STREET: 121 South Righth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 96;
US-09-638-202A-112
Sequence 112, Application US/09638202A
Fatent No. 6462189
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
MUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 361; DB 2; L
Pred. No. 1.9e-35;
4; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APLICATION NUMBER: 09/096,749
APLICATION NUMBER: 09/096,749
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikenine
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,202A
FILING DATE: 11-Aug-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                     ZIP: 55402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77...
Best Tocal Similarity 77...
The T3; Conservative
                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                          STATE: MIN
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; SEQUENCE DESCRIPTION: SEQ ID NO: 112: US-09-637-614-112
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,683A
FILING DATE: 17-UTM-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34, Application US/08078683A Patent No. 5486599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 175 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-078-683A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Patent No. 6703199
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Koiceda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 361; DB 2; Length 96;
Pred. No. 1.9e-35;
4; Mismatches 17; Indels
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                                                                             COMPUTER READABLE FUAL.

MEDIUM TYPE: Diskette
COMPATTING SYSTEM: DOS
SOFTWARE: FASLESQ Version 2.0b
SOFTWARE: FASLESQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749A
FILING DATE: June 12, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1998
PRIOR APPLICATION NUMBER:
FILING DATE: ATORNATION:
NAME: AND S. VIKENINB
REGISTRATION NUMBER: 37,748
REPERBUCE/DOCKET NUMBER: 109.034US1
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATIO
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APPLICATION NUMBER: US/09/637,614
FILING DATE: 11.Aug-2000
PRIOR APPLICATION NUMBER: 09/096,749
FILING DATE: -UNKNOWN-
ATTORNEY/AGENT INPORMATION:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.1%;
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Best Local Similarity 77.78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-096-749A-112
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US-09-637-614-112
COUNTRY:
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3 VSDVPRDLEVVAAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton
APPLICANT: Acto, Masato
ITILE OF INVENTION: Construction and USe of Synthetic
ITILE OF INVENTION: Constructs Encoding Syndecan
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STREET: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Indels
NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REGISTRATION NUMBER: 37,748
REPERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEPHONE: (612) 373-6900
TELEPHONE: (612) 339-3061
INFORMATION FOR SEG ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
73.1%; Score 361; DB 2;
Best Local Similarity 77.7%; Pred. No. 1.9e-35;
Matches 73; Conservative 4; Mismatches 17
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82 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 141
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Patent No. 5302701
GENERAL INFORMATION:
APPLICANT: Hidetaka HASHI et al.
TITIE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 361; DB 2; Length 17
Pred. No. 4.2e-35;
4; Mismatches 17; Indels
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MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,369 FILING DATE: 19921013 CLASSIFICATION: 530 FILING APPLICATION: 530 FILING APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: MUS SP;HOMO SAPIEN
US-09-723-677B-34
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f: U.S.A.
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                                                                                                                                            82 VSDVPRDLEVVAATPTSLIISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 141
                                                                                                                       1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
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                                                   Length 175;
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Pred. No. 4.2e-35;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                            Sequence 34.7—3.7—3.7

Sequence 34.7—3.7—3.7

Patent No. 6531295

GENERAL INFORMATION:

APPLICANT: Saunders, Scott

APPLICANT: Sannders, Scott

APPLICANT: Rato, Masato

TITLE OF INVENTION: Construction and USe of Synthetic

TITLE OF INVENTION: Constructs Encoding Syndecan

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEB: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

CITY: Descon
                                                                                      17; Indels
                                                 Score 361; DB 1;
Pred. No. 4.2e-35;
4; Mismatches 17;
                                                                                                                                                                                                                  142 GLKPGVDYTITVYÁVTGRGDSPASSKPISINYRT 175
                                                                                                                                                                                               61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,683
FILING DATE: 17-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P-41,106
REFERENCE/POCKET NUMBER: CME-062DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,970A
                                               Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
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Best Local Similarity 77.7%;
Matches 73; Conservative
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INFORMATION FOR SEQ 1D NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
; FRAGMENT TYPE: internal US-08-078-683A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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US-08-471-970A-34
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Gaps

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APPLICANT: Hidetaka HASHI et al.
TITE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
STREET: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: In Compatible COMPUTER: In COMPUTER: SOFTWARE: Wordperfect 5.1 CURRENY APPLICATION NUMBER: US/07/959,369 FILING DATE: 19921013 CLASSIPTICATION: 530 PRIOR APPLICATION: 530 PRIOR APPLICATION: APPLICATION: APPLICATION CHARCE: ATTORNEY AGENT INFORMATION: NAME: Warren M. Cheek, JT. REGISTRATION NUMBER: 13,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELECOMUNICATION INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: AMINO ACID
STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: polypeptide
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PEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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TISSUB TYPE:
CELL TYPE:
CELL LINE:
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JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.1%; Score 361; DB 1; Length 256; Best Local Similarity 77.7%; Pred. No. 6.9e-35; Matches 73; Conservative 4; Mismatches 17; Indels
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) FILING DATE:
; FUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-1
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US-07-959-369-10
; Sequence 10. Application US/07959369
; Betent No. 5302701
; GENERAL INFORMATION:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNITS:
PRATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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IMMEDIATE SOURCE:
LIBRARY:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOLUME:
ISSUE:
PAGES:
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DOCUMENT NUMBER: FILING DATE: PUBLICATION DATE:

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Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRICK APPLICATION DATA:
APPLICATION NUMBER: 31721/1994
FILING DATE: 29-NOV-1995
PRICK APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
AND DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
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73.1%; Score 361; DB 1;
Best Local Similarity 77.7%; Pred. No. 7.6e-35;
Matches 73; Conservative 4; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSER: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
GITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: HASHINO=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                             PEATURE:
NAME/KRY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATE:
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
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                                                                                        Score 361; DB 1; Length 258;
Pred. No. 7e-35;
4; Mismatches 17; Indels
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GENERAL INFORMATION:
APPLICANT: Hidetaka HASHI et al.
TITLE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                     217 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 250
                                                                                                                                                                                                                                                                                                                                                                   61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: MEALINGYON

COUNTRY: U.S.A.

ZIP: 20005

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, S.25 inch, 500 kb
COMPUTER: IBM Compatible
OOFRAATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,369
FILING DATE: 19921013
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT:
ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 12, Application US/07959369; Patent No. 5302701
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                   Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: polypeptide
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TYPE: AMINO ACID
STRANDEDNESS: single
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DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
CELL LINE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                    i
US-07-959-369-10
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Query Match 73.1%; Score 361; DB 1; Length 274; Best Local Similarity 77.7%; Pred. No. 7.6e-35; Matches 73; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 628-5197
TELEFAX: (202) 737-3528
TELEFAX: (202) 737-3528
TELEPAX: (202) 737-3528
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
MOLECULE TYPE: peptide
US-08-836-854-3
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Gaps ö

Search completed: February 23, 2006, 07:49:09 Job time: 47 secs

GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.

Copyright

February 23, 2006, 07:59:05

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US-09-688-566-81

Perfect score:

Sequence:

Scoring table:

Searched:

OM protein - protein search, using sw model

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Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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                                Sequence
                    US-10-509-055-15
US-10-486-512-10
US-10-509-055-16
US-09-775-964-5
US-09-775-964-5
US-09-775-964-2
US-10-509-055-17
US-10-509-055-17
US-10-509-055-18
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US-09-775-964-7
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US-09-775-964-8
US-09-775-964-23
                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-486-512-5
US-10-509-055-11
US-09-775-964-24
; Search time 165 Seconds
(without alignments)
238.036 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                       494
1 VSDVPRDLEVVAATPTSRLI......VTDKSDTYKYDDPISINYRT
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Appl Appli 
## ALIGNMENTS

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

1867569 segs, 417829326 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Sequence 1, Application US/10302456;
Publication No. US20030100004A1;
GENERAL INPORMATION:
TITLE OF INVENTION: Solid Phase Immobilization of Proteins;
TITLE OF INVENTION: Solid Poptides
TITLE OF INVENTION: and Peptides
TITLE OF INVENTION: and Peptides
TITLE OF INVENTION: AND TOTAL OF TOTAL ; OTHER INFORMATION: Synthetic Peptide US-10-302-456-1 ORGANISM: Artificial Sequence FEATURE:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length

Score

Result ò N

Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*

61 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS

9

Gaps

1;

Indels

Length 96;

GLKPGVDYTITVYAVTPLRWTETEAHIPIPINYRT 96 61 GLKPGVDYTITVYAVTDKSDT-YKYDDPISINYRT 94

RESULT 2 US-09-096-749A-110

Sequence 110, Application US/09096749A
Fatent No. US20020019517A1
GENERAL INFORMATION:
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA

Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence Sequence

Sequence

Sequence

Sequence Sequence Sequence 1

Sequence

Sequence

14.4%; Score 367.5; DB 4; ilarity 80.0%; Pred. No. 5.8e-34; Conservative 3; Mismatches 15; Query Match Best Local Similarity Matches 76; Conserv Sequence 1, Appli Sequence 110, App Sequence 110, App

Description

Sequence 110, App Sequence 110, App Sequence 3, Appli Sequence 112, App

2 VSDVPRDLEVVAATPTSLLISWKTHEVAARYYRITYGETGGNSPVQEFTVPPWASIATIS ద ð

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Sequence 1 Sequence 1 Sequence 1

Sequence

US-10-302-456-1 US-09-096-749A-110 US-10-174-77A-110 US-10-190-162-110 US-10-190-162-110 US-09-903-412-112 US-09-903-412-112 US-09-903-412-112 US-09-903-412-112 US-10-174-717A-112 US-10-174-717A-112 US-10-174-717A-112 US-10-185-590-2 US-10-185-590-4 US-10-185-590-6 US-10-186-512-1 US-10-186-512-1 US-10-186-512-1 US-10-186-512-1 US-10-186-512-1 US-10-186-512-1

Sequence

Sequence Sequence Sequence

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(612) 373-6900
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INPORMATION FOR SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 94 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: peptide
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US-10-165-155-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VSDVPRDLEVVAATPTSLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 60
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Publication No. US20030108948A1
APPLICANT: Koide, Shohei
TITLE OF INVENTION: ARTHRICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
STREET: 121 South Eighth Street, St. 1600
CITY: Minneapolis
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.1%; Score 361; DB 3; Length 94; Best Local Similarity 77.7%; Pred. No. 3.1e-33; Matches 73; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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APPLICATION NUMBER: US/10/174,717A
FILING DATE: 18-Jun-2002
PRIOR APPLICATION DATA:
                                                                                                COMPUTER: 150 COMPUTED OF STRAILS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/096,749
FILING DATE: June 12, 1998
APPLICATION NUMBER: 60/049,410
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FASESEQ Version 2.0b
                                                                        COMPUTER: IBM Compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: 1
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1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS
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Publication No. US20030134386A1
GENERAL INFORMATION:
APPLICATION: AND APPLICATION: ANTIBODY POLYPEPTIDES
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 112 South Righth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.1%; Score 361; DB 4; Best Local Similarity 77.7%; Pred. No. 3.1e-33; Matches 73; Conservative 4; Mismatches 17
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MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/165,155

FILING DATE: 06-Jun-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/096,749

FILING DATE: June 12, 1998

ATTORNEY/AGENT INFORMATION:

NAME: AID S. VIKERINB

REGISTRATION NUMBER: 37,748

REFERENCE/DOCKET NUMBER: 37,748

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 94
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REGISTRATION NUMBER: 37,748
REPERBNCE/COCKET NUMBER: 109.034US4
TELECOMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEPHONE: (612) 373-6900
TELEPHONE: (612) 33-3061
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
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1 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 60
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REGISTRATION NUMBER: 37,748
REISERNCE/DOCKET NUMBER: 109.034US1
RELEFECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/00/
PRIOR APPLICATION NUMBER: US/09/00/
PRIOR APPLICATION NUMBER: US/09/00/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: June 12
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Publication No. US20030170753A1
GENERAL INPORMATION:
APPLICANT: Koica, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Schwegman, Lundberg, Woesener & Kluth P.A.
STREET: 121 South Bighth Street, Ste. 1600
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Pred. No. 3.1e-33;
4; Mismatches 17; Indels
                                                                                                                                            ch 73.1%; Score 361; DB 4; Length 94; Similarity 77.7%; Pred. No. 3.1e-33; 73; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                        61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DALA:
APPLICATION NUMBER: US/09/096,749
FILING DATE: June 12, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikenins
REGISTRATION NUMBER: 37,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/190,162
FILING DATE: 03-Jul-2002
PRIOR APPLICATION DATA:
                   ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-165-155-110
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SEQUENCE DESCRIPTION: SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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Best Local Similarity 77.7%;
Matches 73; Conservative
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MN
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US-10-190-162-110
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                                                                                                                                                                                     Sequence 3, Application US/10509055
; Publication No. US20050227354A1
; GENERAL INFORMATION:
; APPLICANT: AGAMA, Hiroaki et al.
; TITLE OF INVENTION: PROCESS FOR PRODUCING CYTOTOXIC LYMPHOCYTE
; FILE REFERENCE: 1422-0644PUS1
; CURRENT APPLICATION NUMBER: US/10/509,055
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: PCT/JP03/03575
; RIUGER OF SEQ ID NOS: 24
; SOFTWARE: Patent-In 3.3
; SEQ ID NO 3
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Patent No. US2002019517A1
GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Righth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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Pred. No. 3.2e-33;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                Score 361; DB 3; Length 96; Pred. No. 3.2e-33; 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-903-412-110
; Sequence 110, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/09/903,412
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ 1D NOS: 121
; SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Koide, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
FILE REPERENCE: 109.050USI
CURRENT APPLICATION UNMER: US/09/903,412
CURRENT FILING DATE: 2001-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
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; OTHER INFORMATION: The synthetic Fn3 gene.
US-09-903-412-110
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; Sequence 112, Application US/09903412

; Publication No. US20030027319A1

; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.7%;
Matches 73; Conservative
(612) 373-6900
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Best Local Similarity 77.7%;
Matches 73; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
          TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
                                                                                                                                                                                                                               internal
                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                           ; FRAGMENT TYPE: i
; ORIGINAL SOURCE:
US-09-096-749A-112
                                                                                                                                                                                                         ANTI-SENSE: NO
TELEPHONE:
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LENGTH: 96
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Publication No. US20030108948A1
APPLICANT: Koide, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, St. 1600
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                    Length 96;
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Publication No. US20030027319A1
GENERAL INFORMATION:
APPLICANT: Koids Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
FILE REFERENCE: 109.050US1
CURRENT APPLICATION NUMBER: US/09/903,412
CURRENT FILING DATE: 2001-07-11
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.1%; Score 361; DB 3; 77.7%; Pred. No. 3.2e-33;
                                                                                                                                                                                                                                                                                               Query Match 73.1%; Score 361; DB 3; Best Local Similarity 77.7%; Pred. No. 3.2e-33; Matches 73; Conservative 4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
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PRIOR APPLICATION NUMBER: US 60/217,474
PRIOR FILING DATE: 2000-07-11
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 96
                                                                                                                                                                                                                       ; OTHER INFORMATION: The designed Fn3 gene. US-09-903-412-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 121
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 121
LENGTH: 96
                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 55402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77...
Best Local Similarity 77...
Local 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MIN
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-10-174-717A-112
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US-09-903-412-121
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                                                                                                                                                                                                     FEATURE:
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NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
                                                                                                                                                                                         TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-165-155-112
                                                                                                       INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (612) 339-3061
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SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
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COMPUTER READABLE FORM:
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Best Local Similarity 77...
Best Tocal Similarity 77...
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
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Publication No. US20030134386A1
GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 361; DB 4; Length 96;
Pred. No. 3.2e-33;
4; Mismatches 17; Indels
                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/174,717A
PILING DATE: 18-Jun-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/096,749
FILING DATE: June 12, 1998
APPLICATION NUMBER: 60/049,410
PILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 37,748
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 139-3061
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APPLICATION NUMBER: US/10/165,155
FILING DATE: 06-Jun-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/096,749
FILING DATE: June 12, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
PRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
               COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FASTSEQ Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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MEDIUM TYPE: Diskette
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Matches 73; Conservative
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ZIP: 55402
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3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
                                                           Gaps
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Publication No. US20030170753A1
GENERAL INPORMATION:
APPLICANT: Koleda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 112 South Eighth Street, Ste. 1600
CITY: Minnapolis
STATE: MA
Length 96;
                                                        17; Indels
                                                                                                                 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGET
73.1%; Score 361; DB 4; 77.7%; Pred. No. 3.2e-33; tive 4; Mismatches 17
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COMPUTER: IBM Compatible
SOFTWARE: FastSEQ Version 2.0b
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION NUMBER: US/10/190,162
FILING DATE: 03-Jul-2002
PRIOR APPLICATION NUMBER: US/09/096,749
FILING DATE: June 12, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. VİKBRİLB
REGISTRATION NUMBER: 37,748
REFERRENCE/DOCKET NUMBER: 109.034USI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   63 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
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PRIOR FILING DATE: 1992-03-24
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Job time
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US-10-776-989-34
; Sequence 34, Application US/10776989
; Publication No. US20050075484A1
; GENERAL INFORMATION:
; APPLICANT: SAUUDERS, SCOTT
; APPLICANT: BERNFIELD, MERTON
; APPLICANT: RATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-232
; CURRENT APPLICATION NUMBER: US/10/776,989
; CURRENT FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/471,970
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1993-06-06
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
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TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF
FILE REPERBYCE: 176/60901
CURRENT APPLICATION NUMBER: US/10/006,760
CURRENT APPLICATION NUMBER: 001-11-19
PRIOR APPLICATION NUMBER: 60/249,756
PRIOR APPLICATION NUMBER: 2001-11-17
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PARCHIN Ver: 2.1
SEQ ID NO 2
LENGTH: 96
                                                                                                                                                                                                                                                                                       1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                                                                                                                                                                                                                                                                                                     3 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 62
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                                                                                                                                                                                 Query Match 73.1%; Score 361; DB 4; Length 96; Best Local Similarity 77.7%; Pred. No. 3.2e-33; Matches 73; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                               61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                             63 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 96
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                   ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-190-162-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10006760 Publication No. US20030186385A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Homo sapiens
US-10-006-760-2
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-10-006-760-2
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1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
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                                                                                                                                                                                                                                                                                                                          Length 175;
                                                                                                                                                                                                                                                                                                                   Score 361; DB 5; Length 17
Pred. No. 6.7e-33;
4; Mismatches 17; Indels
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ne : 166 secs
PRIOR APPLICATION UNMER: 07/757,654
PRIOR FILING DATE: 1991-09-06
PRIOR FILING DATE: 1991-09-16
PRIOR FILING DATE: 1991-09-12
PRIOR FILING DATE: 1991-03-12
PRIOR PILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
LENGTH: 175
TYPE: PRI
ORGANISM: MUS SP;HOMO SAPIEN
US-10-776-989-34
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.7%;
Matches 73; Conservative
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us-09-688-566-81.rapbn

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; Search time 42 Seconds
(without alignments)
33.319 Million cell updates/sec
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1 VSDVPRDLEVVAATPTSRLI.....VTDKSDTYKYDDPISINYRT
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1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO8

4: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/DCT NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USI0_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USI1 NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USI1 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             117670 seqs, 14887254 residues
                                                                                                                                                          February 23, 2006, 08:01:29
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                      US-09-688-566-81
                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 25, Appl	Sequence 29, Appl	Sequence 4, Appli	ď,	Sequence 22, Appl	7,	Sequence 21, Appl	8	23	24	14	63,	Sequence 625, App	Sequence 628, App	63	62	62	Sequence 25, Appl	25	Sequence 25, Appl	25	Sequence 25, Appl	Sequence 38, Appl	Sequence 38, Appl	38,
SUMMARIES		er	US-11-181-091-25	US-11-181-091-29	US-11-181-091-4	US-11-181-091-5	US-11-181-091-22	US-11-181-091-7	US-11-181-091-21	US-11-181-091-8	US-11-181-091-23	US-11-181-091-24	US-11-181-091-14	US-10-995-561-634	US-10-995-561-625	US-10-995-561-628	US-10-995-561-630	US-10-995-561-621	US-10-995-561-624	US-11-193-561-25	US-11-193-771-25	US-11-193-789-25	US-11-193-806-25	US-11-193-857-25	US-11-193-561-38	US-11-193-771-38	US-11-193-789-38
		<b>图</b> :	7	7	7	7	7	7	7	7	7	7	7	9	9	ø	9	9	9	7	7	7	7	7	2	7	7
		Match Length DB	274	302	432	457	457	464	472	489	549	574	826	847	1259	1286	1315	1341	1348	2176	2176	2176	2176	2176	2217	2217	2217
æ	Query	Match	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1
		Score	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361	361
	Result	No.	1	7	ю	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 38, Appl Sequence 33, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 627, Appl Sequence 627, Appl Sequence 627, Appl Sequence 627, Appl Sequence 627, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl	
US-11-193-806-38 US-11-193-857-38 US-11-193-561-633 US-11-193-761-23 US-11-193-771-23 US-11-193-806-23 US-11-193-807-23 US-11-193-807-23 US-11-193-807-21 US-11-193-807-21 US-11-193-807-21 US-11-193-807-19 US-11-193-807-19 US-11-193-807-19 US-11-193-807-19 US-11-193-807-19 US-11-193-807-19	
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2217 2217 2217 2217 2296 2296 2296 2330 2330 2330 2355 2355 2355 2355 2355	
361 361 361 361 361 361 361 361 361 361	
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ALIGNMENTS

RESULT 1 US-11-181-091-25 Sequence 25, Application US/11181091 Publication No. US20060030046A1 GENERAL INFORMATION: APPLICANT: Asada, Kiyozo GENERAL INFORMATION: HOWOTI, Takashi KOyama, Nobuto Hashino, Kimikazu Kacyama, Nobuto Hashino, Kimikazu Kaco, Ikunoshin TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET CELLS WITH RETROVIRUS NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: WEISER & ASSOCIATES STREET: 230 SOUTH FIfteenth Street, Suite 500 CITY: Philadelphia		
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US-11-181-091-4
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Publication No. US20060030046A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AGGAG, Kiyozo
UGenori, Takashi
Koyama, Nobuto
Habhino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
                                                                                                                                                                                                                     73.1%; Score 361; DB 7; Length 274; 77.7%; Pred. No. 4.4e-32;
                                                                                                                                                                                                                                                                 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                        238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
                                                                                                                                                                                                                                                                                                                                                                                             61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATLING DATE: 20-Peb-2001

PILING DATE: 20-Peb-2001

APPLICATION NUMBER: US/09/366,009

FILING DATE: 02-Aug-1999

APPLICATION NUMBER: 08/809,156

FILING DATE: -UNFONN

APPLICATION NUMBER: JP 294382/1995

FILING DATE: 13-NOV-1995

FILING DATE: 08-MAR-1996

ATTONNEY/AGENT: NOFRMARTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-U1-2005
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                         Local Similarity 77.7 tes 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                            US-11-181-091-25
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US-11-181-091-29
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178 VSDVPRDLEVVAATPISLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 237
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Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FIOPPY GISK
MEDIUM TYPE: FIOPPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-Jul-2005
CLASSIFCATION INDERS: US/09/75,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: US/09/366,009
FILING DATE: CO-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: CO-Feb-2001
APPLICATION NUMBER: US/09/156
FILING DATE: UNANOWN-
APPLICATION NUMBER: US/09/1996
FILING DATE: 13-NOV-1995
ATONNEY/AGENT INFORMATION:
NAME: Webiser: Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 19,763
TELEPHONE: 215-875-8383
                                                                                                                                                                                               Length 302;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                          73.1%; Score 361; DB 7;
77.7%; Pred. No. 4.9e-32;
tive 4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                           ;
STRANDEDNESS: «Unknown»
;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-11-181-091-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; USMORIA USAGAI
; USMORIA USAGAI
; KOYAMA, NObuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
LENGTH: 302 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 432 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 215-875-8394 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19102
COMPUTER READABLE FORM:
                                                                                                                                                                        Query Match
Best Local Similarity 77.77
Best Local Similarity 77.77
Conservative
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COUNTRY: USA
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RESULT
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                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET CELLS WITH RETROVIRUS
                                                                                                                     Score 361; DB 7; Length 432;
Pred. No. 7.5e-32;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER KEALABLE FOURT

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091

FILING DATE: 14-Jul-2005

CLASSIFICATION NUMBER: US/09/75,964

FILING DATE: 20-Peb-2001

APPLICATION NUMBER: US/09/366,009

FILING DATE: 02-Aug-1999

APPLICATION NUMBER: 08/09/366

APPLICATION NUMBER: 07 294382/1995

FILING DATE: 13-NOV-1995

APPLICATION NUMBER: JP 051847/1996

FILING DATE: 13-NOV-1996

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                 238 GLKPGVDYIITVYAVTGRGDSPASSKPISINYRT 271
                                                                                                                                                                                                                                                                                           61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
    TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-181-091-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                               US-11-181-091-5

Sequence 5, Application US/11181091

Publication No. US20060030046A1

GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koyama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uemori, Takashi
Ueno, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                     Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                        Gaps
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Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
                                                                                          DB 7; Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
                                                                                          73.1%; Score 361; DB 7; L 77.7%; Pred. No. 8e-32; tive 4; Mismatches 17;
                                                                                                                                                                                                                                                                                                      238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
                                                                                                                                                                                                                                                                           61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: «Unknown:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATE:
FILING DATE: 14-Jul-2005
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 977.6507P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: Jinear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-181-091-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-975-8383
TELEPAX: 215-876-8394
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
UFFICANT: UFFICANT: UFFICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uenori, Takashi
Ueno, Takashi
Koyama, Nobuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 39
                                                                  Query Match
Best Local Similarity 77, ...
Best Local 3 Conservative
73; Conservative
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RESULT
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                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/11181091
Sequence 7, Application US/20060030046A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Takashi
Ueno, Takashi
Ueno, Takashi
Kato, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: CELLS WITH RETROVIRUS
                                              DB 7; Length 457;
                                         Score 361; DB 7; Length 45:
Pred. No. 8e-32;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-Jul-2005
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                   238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
                                                                                                                                                                                                                         61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/99/775,964
FILING DATE: 20.Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: 4UAROWN-SPER: 08/809,156
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 294382/1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-11-181-091-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 464 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
                                           Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19102
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
JS-11-181-091-22
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US-11-181-091-7
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                                                                                                                             178 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 237
                                                                                              1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
  Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 472;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: WEISER & ASSOCIATES
STRET: 230 South Fifteenth Street, Suite 500
STATE: Philadelphia
STATE: PA
Score 361; DB 7; Le
Pred. No. 8.1e-32;
4; Mismatches 17;
                                                                                                                                                                                                                  61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: END PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONTURENT APPLICATION DATE: 14-701-2005
FILING DATE: 14-701-2005
PRIOR APPLICATION CONTUREN: US/09/775,964
FILING DATE: 20-Reb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: US/09/366,009
FILING DATE: COMPG-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: COMPG-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 13-NOV-1995
FILING DATE: 13-NOV-1995
FILING DATE: 13-NOV-1995
FILING DATE: 108-MAR-1996
ATTORNEY/AGRNT NNFORMETON
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Pred. No. 8.3e-32;
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REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
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) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-11-181-091-21
                                                                                                                                                                                                                                                                                                                       US-11-181-091-21
Sequence 21, Application US/11181091
Publication No. US20060330046A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: 215-875-8383 TELEFAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                           Uemori, Takashi
Ueno, Takashi
Koyama, Nobuto
                                                                                                                                                                                                                                                                                                                                                                                                                                           Takashi
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Query Match 73.1%;
Best Local Similarity 77.7%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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Best Local Similarity
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178 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 237
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CELLS WITH RETROVINGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091

FILING DATE: 14-Jul-2005

CLASSIFCATION: cUnknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/75,964

FILING DATE: 20-Feb-2001

APPLICATION NUMBER: US/09/366,009

FILING DATE: 02-Aug-1999

APPLICATION NUMBER: 08/809,156

FILING DATE: CUNKNOWN>

APPLICATION NUMBER: JP 294382/1995

FILING DATE: 13-NOV-1995

APPLICATION NUMBER: JP 051847/1996

FILING DATE: 08-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
73.1%; Score 361; DB 7;
Best Local Similarity 77.7%; Pred. No. 9.8e-32;
Matches 73; Conservative 4; Mismatches 17;
                                                                                                         GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-11-181-091-23
                                                                                                                                                                                                                                 Sequence 23, Application US/11181091; Publication No. US20060030046A1; GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 549 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 23:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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                                                                 1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                       Habhino, Kimikazu
Habhino, Ikunoshin
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.1%; Score 361; DB 7; Length 489; 77.7%; Pred. No. 8.6e-32; Live 4; Mismatches 17; Indels
17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                      238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
                                                                                                                              GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-701-2005
CLASSIFICATION: «UNKNOWN-
PRIOR APPLICATION ATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-F6b-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-AUG-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 07-995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 08-MRA: 1996
4; Mismatches
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REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-11-181-091-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                           Sequence 8, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 489 amino acids TYPE: amino acid
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Ueno, Takashi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19102
UTER READABLE FORM:
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Best Local Similarity 77.7
Matches 73; Conservative
73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF
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                                                                                                                              61
Matches
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1 VSDVPRDLEVVAATPTSRLISWNRSGLQSRYYRITYGETGGNSPVQEFTVPPWASIATIS 60
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Publication No. US20060030046A1
GENERAL INFORMATION:
APPLICANT: Fadada, Kiyozo
Uemo, Takashi
Uemo, Takashi
Kayama, Nobuto
Hashino, Kimikazu
Kato, Ikunsahin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 826;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                        238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
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Pred. No. 1.6e-31;
4; Mismatches 17
61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GLKPGVDYTITVYAVTDKSDTYKYDDPISINYRT 94
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APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-UU1-2005
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-Aug-1999
PPILCATION NUMBER: 08/809,156
FILING DATE: «UNKNOWN:
APPLICATION NUMBER: JP 294382/1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: «Unknown»
TOPOLGGY: linear
MOLECULE TYPE: peptide
SRQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
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77.78;
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Best Local Similarity 77. (*)
Conservative
The T3; Conservative
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                                                                                                            RESULT 11
JS-11-181-091-14
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178 VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATIS 237
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Robito
Robito, Kimikazu
Rato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7; Length 574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-Jul-2005
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                            238 GLKPGVDYTITVYAVTGRGDSPASSKPISINYRT 271
                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/775,964
APPLICATION NUMBER: US/09/366,009
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: US/09/156
FILING DATE: US/09/196
FILING DATE: US/09/1995
FILING DATE: US/09/1995
FILING DATE: US/09/1995
FILING DATE: US/09/1995
FILING DATE: US/09/1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
TELEPHONE: 215-875-8383
TELEPAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       Sequence 24, Application US/11181091
Publication No. US20060030046A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               APPLICANT: Asada, Kiyozo
Uemori, Takashi
                                                                                                                                                                                                                                                                                 Uemori, Takas
Ueno, Takashi
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Best Local Similarity 77.7%;
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19102
                                                                                                                                                                    US-11-181-091-24
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LENGTH: 1315
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                                                                                Sequence 634. Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL. Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DESCRICT AND USES THEREOF
TITLE OF INVENTION: DESCRICT AND USES THEREOF
TITLE OF INVENTION DATE: 2004-11-24
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 634
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| Publication No. US20050272054A1
| GENERAL INFORMATION:
| APPLICART: CREGILL, Michele et al. |
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH ITTLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF |
| TITLE OF INVENTION: DATECTION AND USES THEREOF |
| TITLE OF INVENTION: DATECTION AND USES THEREOF |
| CURRENT APPLICATION NUMBER: US/10/995,561 |
| CURRENT PILING DATE: 2004-11-24 |
| NUMBER OF SEQ ID NOS: 85702 |
| SOFTWARE: PASECREO FOR Mindows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.1%; Score 361; DB 6; Length 847; llarity 77.7%; Pred. No. 1.6e-31; Conservative 4; Mismatches 17; Indels
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Best Local Similarity 77.7%
Matches 73, Conservative
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US-10-995-561-634
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 73; Conserv
                                                         RESULT 12
US-10-995-561-634
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US-10-995-561-628 ; Sequence 628, Application US/10995561 ; Publication No. US20050272054A1

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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: 18/10/995, 561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 628
LENGTH: 1286
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Publication No. US20050272054A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFURMER: PastSEQ for Windows Version 4.0
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Pred. No. 2.7e-31;
4; Mismatches 17
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Best Local Similarity 77.74
Matches 73; Conservative
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US-10-995-561-630
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Best Local Similarity
Matches 73; Conserv
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